

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Om protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2003, 12:44:54 ; Search time 1420 Seconds
(without alignments)
1129.122 Million cell updates/sec

Title: US-09-801-115B-2
Perfect score: 508
Sequence: 1 MDNWPQPKIHRPFCFSVKGH.....LENPSGPYQQKKPVHEKREV 99
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 16154066 seqs, 809743376 residues
Total number of hits satisfying chosen parameters: 32308132
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn_2_1/USPITO_spool/_US0980115/runat_20062003_141103_13596/app_query.fasta_1.263
-DB=EST -QRFN=fastap -SUFIX=_rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40_cdi -LIST=45
-DOCALIGN=200 -THR_SCORE_PCT = THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFILE=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0980115 @CGN_1-1_2874_@runat_20062003_141103_13596 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERIES -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARM_TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPOP=6
-FGAPEXT=7 -YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

No.	Score	Query	%	Match	Length	DB	ID	Description
c 1	508	100.0	386	9	AA911088			AA911088 ok67e01.s
c 2	508	100.0	391	9	A1987739			A1987739 w21e10.x
c 3	508	100.0	396	10	AW83193			AW83193 x116f11.x
c 4	508	100.0	399	9	AA516431			AA516431 ne58a03.s
c 5	508	100.0	402	9	A1987747			A1987747 w21f09.x
c 6	508	100.0	404	13	BM53628			BM53628 agencn02.x
c 7	508	100.0	409	9	AI826623			AI826623 w3d5d10.x
c 8	508	100.0	423	9	A118804			A118804 qaf4b08.s
c 9	508	100.0	427	9	AA45042			AA45042 aa04a707.s
c 10	508	100.0	432	9	AA429945			AA429945 zw67f10.s
c 11	508	100.0	452	9	A1078580			A1078580 ox2zh05.x
c 12	508	100.0	453	9	A1743235			A1743235 w3g9a02.s
c 13	508	100.0	458	12	BF109912			BF109912 717f03.x
c 14	508	100.0	510	12	BF309486			BF309486 UI-R-Cai-
c 15	508	100.0	524	12	BG705303			BG705303 602687808
c 16	508	100.0	534	12	BG31757			BG31757 602299819
c 17	505	99.4	487	13	BM472086			BM472086 AGENCN02
c 18	504	99.2	386	9	AA983129			AA983129 ox75h10.s
c 19	504	99.2	781	12	BG29972			BG29972 602579169
c 20	504	99.2	962	12	BG29994			BG29994 602246262
c 21	491	96.7	529	12	BG691818			BG691818 602247787
c 22	484	95.3	443	12	BG613984			BG613984 602641513
c 23	480	94.5	432	10	AV59888			AV59888 AV759888
c 24	476.5	93.8	395	9	A1141284			A1141284 qa5ch10.s
c 25	475	93.5	353	9	A1265924			A1265924 qx60d08.x
c 26	475	93.5	930	12	BF203359			BF203359 qd186596
c 27	472	92.9	468	14	W52820			W52820 xc55c06.rl
c 28	471.5	92.8	527	9	AA875339			AA875339 oexbh08.s
c 29	471.5	92.8	534	14	BQ130559			BQ130559 l188a05.x
c 30	471.5	92.8	534	14	BQ13826			BQ13826 l116a04.x
c 31	471.5	92.8	551	9	AA702011			AA702011 z17od2.s
c 32	471.5	92.8	692	11	AF151058			AF151058 Homo sapi
c 33	471.5	92.8	776	10	AV683453			AV683453 AV683453
c 34	471	92.7	409	14	N89912			N89912 zb22909.s1
c 35	467.5	92.0	789	12	BQ7159			BQ7159 60130591
c 36	465.5	91.6	542	14	BQ129993			BQ129993 1.82h06.x
c 37	463	91.1	543	12	BG53587			BG53587 602562152
c 38	460.5	90.6	678	13	BT151562			BT151562 AA987264 os11a06.s
c 39	459	89.0	333	9	AA98264			AA98264 os11a06.s
c 40	445.5	87.7	500	9	AI633679			AI633679 th1c04.x
c 41	445.5	87.7	654	12	BP791773			BP791773 602704973
c 42	444	87.4	326	9	A126361			A126361 q62bd12.x
c 43	442.5	87.1	606	14	W93646			W93646 zd97d08.s1
c 44	436	85.8	456	12	BE875161			BE875161 6014875161
c 45	435	85.6	319	9	AI349474			AI349474 qpt2f07.x

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ORGANISM	DEFINITION	ORGANISM
1	AA911088/C	AA911088	386 bp mRNA	mRNA	linear
					EST 09-TUN-1998
					IMAGE:1519032 3'
					DEFINITION
					mRNA sequence.
					DEFINITION
					AA911088
					ACCESSION
					AA911088.1
					VERSION
					EST
					SOURCE
					Homo sapiens
					ORGANISM
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
					Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo;
					REFERENCE
					1 (bases 1 to 386)
					REFERENCE
					NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
					AUTHORS
					TITLE
					National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

ACCESSION	IMAGE:2662317 3', mRNA sequence.
VERSION	AWI83193
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-re@mail.nih.gov
FEATURES	This clone is available royalty-free through LILN ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
source	Seq primer: #40UP from Gibco. Location/Qualifiers 1. .396 /organism="Homo sapiens" 'db_xref="taxon:9606" 'clone="IMAGE:2662317" 'clone_1_id="Soares_NEL_T_GBC_S1" 'lab_host="DH10B" 'note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NB119W, testis NIH, and B-cell NCI CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 274480-3/02087, 682632-6/87239, I.M.A.G.E. clones 728711, and 729086-7/31399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT	115 a 92 c 80 g 109 t
ORIGIN	Alignment Scores: Pred. No.: 4.24e-59 Length: 396 Score: 508.00 Matches: 99 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: Gaps: 0
BASE COUNT	US-09-801-115B-2 (1-99) x AWI83193 (1-396)
ORIGIN	QY 1 MetaspasValGlnProLysIleArgIleGlySerValLeuGlyHis 20 Db 359 ATGGATAACGGTCAGCCGAAATTAACAGATCGCCCTCTGCCTCAGTGAAAGGCCAC 300 QY 21 ValLeuMetLeuArgLeuAspIleLeuSerLeuValThrValPheLeuLeu 40 Db 299 GTGAGATGCTGCGCTGATATTCAGTCACTCTGGAACAGTCATGCATC 240 QY 41 ValSerValLeuLeuLeuLeuProGluThrThrLeuThrValGlyGlyValLeu 60 Db 239 GТАCTGTGCTGGCACTCATCCAGAACACACATGACAGTTGGAGGGCTT 180 QY 61 AlaLeuValThrAlaValCysCysLeuLeuAspGlyAlaLeuLeuLeuLeu 80 Db 179 GCACTTGACAGCAGTAGCTGCTGCTCCGACGGGGCCATTATCCGGAGCTCTG 120 QY 81 PheAsnProSerGlyProArgGlyLysLysProValHisGluLysLysGluValLeu 99 Db 119 TTCAATCCAGCGCTCTTACCAAGAAAAGCCAGTGTGATGAAAGAAGCTTGT 63 RESULT 4 AS16431/c LOCUS AA516431 OY 399 bp mRNA linear EST 13-AUG-1997
DEFINITION	ne58a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:901516 3', mRNA sequence.
ACCESSION	AA516431
VERSION	AA516431.1 GI:2255955
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-re@mail.nih.gov
FEATURES	Tumor Gene Index
source	Seq primer: -40m13 fwd. ET from Amersham. Location/Qualifiers 1. .399 /organism="Homo sapiens" 'db_xref="taxon:9606" 'clone="IMAGE:901516" 'clone_1_id="NCI_CGAP_Co3" 'sex="pooled" 'tissue_type="colon" 'lab_host="DH10B" 'note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3D vector. Library went through one round of normalization." DB: Gaps: 0
BASE COUNT	115 a 94 c 81 g 109 t
ORIGIN	Alignment Scores: Pred. No.: 4.28e-59 Length: 399 Score: 508.00 Matches: 99 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: Gaps: 0
BASE COUNT	US-09-801-115B-2 (1-99) x AA516431 (1-399)
ORIGIN	QY 1 MetaspasValGlnProLysIleArgIleGlySerValLeuGlyHis 20 Db 357 ATGGATAACGGTCAGCCGAAATTAACAGTCAGTGAAAGGCCAC 298 QY 21 ValLeuMetLeuArgLeuAspIleLeuSerLeuValThrValPheLeuLeu 40 Db 297 GTGAGATGCTGCGCTGATATTCAGTCACTCTGGAACAGTCATGCATC 238 QY 41 ValSerValLeuLeuLeuLeuProGluThrThrLeuThrValGlyGlyValLeu 60 Db 237 GТАCTGTGCTGGCACTCATCCAGAACACACATGACAGTTGGAGGGCTT 178 QY 61 AlaLeuValThrAlaValCysCysLeuLeuAspGlyAlaLeuLeuLeuLeu 80 Db 177 GCACCTGTGACAGCAGTAGCTGCTGCTCCGACGGGGCCATTATCCGGAGCTC 118 QY 81 PheAsnProSerGlyProArgGlyLysLysProValHisGluLysLysGluValLeu 99

Db	117	TTCATCCAGGGTCTTACAGAAAGCTGATGAAAAAAGAAGTTTG	61	AilieuvauThrialavalCyscysLeuilaAspGlyAlaLeuIleTrArgysLeuIe 80
RESULT	5	AT989747/c	IMAGE:2520713 3', mRNA sequence.	GCATGTGACACAGTCTGCTGCCAGGGCCCTATTACCGGAAGCTCTG 129
DEFINITION		W21f09.x1 Soares-Dieckgraefe_colon_NHEC	Homo sapiens cDNA clone	81 PhasenProSerGlyProTyroGlylysProValHsGluIysGluIleu 99
LOCUS	AT989747	402 bp	mRNA linear EST 27-oct-1999	128 TTCATCCAGGGTCTTACAGAAAGCTGATGAAAAAAGAAGTTTG 72
VERSION	AT989747			
SOURCE	EST			
ORGANISM	human			
JOURNAL	Bukarwota			
COMMENT	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Unpublished (1997)			
AUTHORS	Mammalia; Butheria1; Primates; Catarhini; Hominidae; Homo. (bases 1 to 402)			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
FEATURES	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), tumor Gene Index			
source	Contact: Robert Strausberg, Ph.D.			
	Email: cgsabs@mail.nih.gov			
	This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.			
	Seq primer: -40bp from Gibco.			
	Location/Qualifiers			
	1..402			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:2520713"			
	/tissue_type="colonic mucosa from 3 patients with Crohn's disease"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Organ: colon; Vector: pMT73-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TCTTACCACTTGTGACTGGAGCGCGCTCTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I vector. Eco RI sites of the modified pMT73 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieckgraef.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. library constructed by Bentor soares and M. Fatima Bonaldo."			
BASE COUNT	113	a 90 c 82 g 117 t		
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Alignment Scores:				
Prep. No.:	4.33e-59	Length:	402	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	9	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
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DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
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Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
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Percent Similarity:	100.00%	Conservative:	0	
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Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
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DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
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Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
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DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
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Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
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Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
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Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
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DB:	13	Gaps:	0	
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Prep. No.:	4.36e-59	Length:	404	
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Percent Similarity:	100.00%	Conservative:	0	
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DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121	a 80 c 87 g 116 t		
ORIGIN				
Alignment Scores:				
Prep. No.:	4.36e-59	Length:	404	
Score:	508.00	Matches:	99	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	13	Gaps:	0	
BASE COUNT	121</			

QY	61	AlaIeuvalthrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuIle 80	Db	307	GTCAGAGAGCTGGGGCTGATATACTCACTACTGTAAACACAGATTATGCATGTCATC 24
Db	212	GCACTTGtgacAGCAGTGCTGCTGCTGCGACGGGCCCTTAATACGGAAAGCTCTG 271	QY	41	Va3SerValLeuAlaLeuIleProGluLhrThrThrLeuThrValGlyGlyGlyValPhe 60
Db	212	GCACTTGtgacAGCAGTGCTGCTGCTGCGACGGGCCCTTAATACGGAAAGCTCTG 271	Db	247	GTACtGtGttGGAAGTACAGAAGAACACACATGACAGTGTGGAGGGGTT 188
QY	81	PheAsnProSerGlyProTyroGlyLysProValHisGluLysGluValLeu 99	QY	61	AlaIeuvalthrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuIle 80
Db	272	TTCATCCAGCCTCTTACAGAAAGCCTGCTGCTGAGAAAGTGTG 328	Db	187	GCACTTGtgacAGCAGTGCTGCTGCGACGGGCCCTTAATACGGAAAGCTCTG 128
QY	1	MetAspAsnValGlnProLysIleGlyHisArgProPheCysPheSerValLysGlyHis 20	QY	81	PheAsnProSerGlyProTyroGlyLysProValHisGluLysGluValLeu 99
Db	367	ATGGAAACGGCAGCGGAAATAACATGCGCCCTCTGCTGCTGAGAAAGCCAC 308	Db	127	TTCATCCAGCCTCTTACAGAAAGCCTGCTGAGAAAGTGTG 71
QY	21	VallysMetLeuArgLeuAspLeuAsnSerLeuValThrThrValPhenMetLeuIle 40	QY	1	MetAspAsnValGlnProLysIleGlyHisArgProPheCysPheSerValLysGlyHis 20
QY	RESULT	7	AI26623/c	COMMENT	AI12804/c
LOCUS	AI26623	409 bp	mRNA	linear	EST 21-DEC-1999
DEFINITION	AI26623.1	NCI_CGAP_Pr22	Homo sapiens	cDNA clone	IMAGE:2417395 3',
VERSION	A1826623				
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens				
COMMENT	human.				
EST.					
JOURNAL					
CONTACT	Robert Strausberg, Ph.D.				
Email:	cgbps-r@mail.nih.gov				
Tissue Procurement:	Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.				
CDNA Library Preparation:	M. Bento Soares, Ph.D.				
CDNA Library Arrayed by:	Greg Lennon, Ph.D.				
DNA Sequencing by:	Washington University Genome Sequencing Center				
Clone distribution:	NCI-CGAP clone distribution information can be found through the J.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/bhrp/Image/Image.html				
Insert Length:	462	Std Error:	0.00		
Seq primer:	-40UP from Gibco.				
FEATURES					
source					
1.	409				
/organism="Homo sapiens"					
/db_xref="taxon:9606"					
/clone_1.lib="NCI_CGAP_Pr22"					
/sex="male"					
/tissue_type="normal prostate"					
/lab_host="Bnl10B"					
/note="Organ: prostate; Vector: pT7TD-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7M3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."					
BASE COUNT	112	a 94 c 80 g 123 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.44e-59	Length:	409		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00	Matches:	99		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	9	Indels:	0		
DB:		Gaps:	0		
BASE COUNT	116	a 101 c 89 g 117 t			
ORIGIN					
Alignment Scores:					
Pred. No.:	4.66e-59	Length:	423		
Score:	508.00				

Db	353	ATGGATAACGTGAGCCGAAATAAACATGCCCTCTGCCTCAGTGGAAAGGCAC	294	Pred. No.: 4	4.72e-59	Length: 427
Qy	21	VallysMetleurgLeAspIleleasnserleuvalthrhrvaPhenetylleile	40	Score: 50.8.00	Matches: 99	
Qy	21	VallysMetleurgLeAspIleleasnserleuvalthrhrvaPhenetylleile	40	Percent Similarity: 100.00%	Conservative: 0	
Qy	21	VallysMetleurgLeAspIleleasnserleuvalthrhrvaPhenetylleile	40	Best Local Similarity: 100.00%	Mismatches: 0	
Db	293	GTGAGAAGCTGGCTGCGTSGATATTCACACTCTG	234	Query Match: 100.00%	Indels: 0	
Qy	41	ValSerValLeuAlaLeuLeProGluThrThrLeuThrValGlyGlyGlyValPhe	60	Query Match: 9	Gaps: 0	
Qy	41	ValSerValLeuAlaLeuLeProGluThrThrLeuThrValGlyGlyGlyValPhe	60	Organism: Homo sapiens		
LOCUS	AA455042/c	AA455042	427 bp	mRNA	linear	EST 06-JUN-1997
DEFINITION	Soares_NHMPU_S1	Homo sapiens	cDNA clone	IMAGE:812244		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA455042.1	GR:2177818				
TITLE	WashU-Merck EST Project 1997					
JOURNAL	Unpublished (1997)					
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu					
FEATURES	/organism="Homo sapiens" /db_xref="GDB:6043155" /db_xref="taxon:9606" /clone="IMAGE:812244" /clone_lib="Soares_NHMPU_S1" /tissue_type="pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH10B"					
/note="Organ: mixed (see below); Vector: pTT3D-Pac						
Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NbH19W, and fetal heart NbH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of T.M.A.G.E. clones 260232-265223, 340488-345479, and 484188-489479."						
BASE COUNT	119	a	101	c	91	g
ORIGIN						
Alignment Scores:						
RESULTS	9					
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA455042		
Qy	173	GCACGTGAGCACAGCATGCTGCTTGCCGACGGGCGCTTATTACGGAGCTCTG	114	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA455042.1		
Qy	113	TTCATTCAGCGGCTCTTACCGAGAAAGCCCTGCTGATGAAAAGAGAGTTG	57	Version: GR:2177818		
Qy	41	ValSerValLeuAlaLeuLeProGluThrThrLeuThrValGlyGlyGlyValPhe	60	Title: WashU-Merck EST Project 1997		
Qy	41	ValSerValLeuAlaLeuLeProGluThrThrLeuThrValGlyGlyGlyValPhe	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA455042		
Qy	21	VallysMetleurgLeAspIleleasnserleuvalthrhrvaPhenetylleile	40	Definition: mRNA sequence.		
Qy	21	VallysMetleurgLeAspIleleasnserleuvalthrhrvaPhenetylleile	40	Accession: AA455042.1		
Qy	296	GTGAGATGCTCGGGCTGATATATCACTACTGTAACAGTACATGCTCATC	237	Version: GR:2177818		
Qy	41	ValSerValLeuAlaLeuLeProGluThrThrLeuThrValGlyGlyGlyValPhe	60	Title: WashU-Merck EST Project 1997		
Qy	41	ValSerValLeuAlaLeuLeProGluThrThrLeuThrValGlyGlyGlyValPhe	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA455042		
Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA455042.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2177818		
RESULTS	10					
Qy	AA429945/c	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429945	AA429945				
DEFINITION	zwf10.s1 Soares_testis_NHT	Homo sapiens	cDNA clone	IMAGE:781291		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA429945.1	GR:2113244				
KEYWORDS	EST.					
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Title: WashU-Merck EST Project 1997		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA429945		
Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA429945.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2113244		
RESULTS	10					
Qy	AA429945/c	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429945	AA429945				
DEFINITION	zwf10.s1 Soares_testis_NHT	Homo sapiens	cDNA clone	IMAGE:781291		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA429945.1	GR:2113244				
KEYWORDS	EST.					
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Title: WashU-Merck EST Project 1997		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA429945		
Qy	21	VallysMetleurgLeAspIleleasnserleuvalthrhrvaPhenetylleile	40	Definition: mRNA sequence.		
Qy	21	VallysMetleurgLeAspIleleasnserleuvalthrhrvaPhenetylleile	40	Accession: AA429945.1		
Qy	296	GTGAGATGCTCGGGCTGATATATCACTACTGTAACAGTACATGCTCATC	237	Version: GR:2113244		
Qy	41	ValSerValLeuAlaLeuLeProGluThrThrLeuThrValGlyGlyGlyValPhe	60	Title: WashU-Merck EST Project 1997		
Qy	41	ValSerValLeuAlaLeuLeProGluThrThrLeuThrValGlyGlyGlyValPhe	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA429945		
Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA429945.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2113244		
RESULTS	10					
Qy	AA429945	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429945	AA429945				
DEFINITION	zwf10.s1 Soares_testis_NHT	Homo sapiens	cDNA clone	IMAGE:781291		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA429945.1	GR:2113244				
KEYWORDS	EST.					
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Title: WashU-Merck EST Project 1997		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA429945		
Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA429945.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2113244		
RESULTS	10					
Qy	AA429945	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429945	AA429945				
DEFINITION	zwf10.s1 Soares_testis_NHT	Homo sapiens	cDNA clone	IMAGE:781291		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA429945.1	GR:2113244				
KEYWORDS	EST.					
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Title: WashU-Merck EST Project 1997		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA429945		
Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA429945.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2113244		
RESULTS	10					
Qy	AA429945	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429945	AA429945				
DEFINITION	zwf10.s1 Soares_testis_NHT	Homo sapiens	cDNA clone	IMAGE:781291		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA429945.1	GR:2113244				
KEYWORDS	EST.					
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Title: WashU-Merck EST Project 1997		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Journal: Unpublished (1997)		
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Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA429945		
Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA429945.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2113244		
RESULTS	10					
Qy	AA429945	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429945	AA429945				
DEFINITION	zwf10.s1 Soares_testis_NHT	Homo sapiens	cDNA clone	IMAGE:781291		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA429945.1	GR:2113244				
KEYWORDS	EST.					
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Title: WashU-Merck EST Project 1997		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA429945		
Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA429945.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2113244		
RESULTS	10					
Qy	AA429945	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429945	AA429945				
DEFINITION	zwf10.s1 Soares_testis_NHT	Homo sapiens	cDNA clone	IMAGE:781291		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA429945.1	GR:2113244				
KEYWORDS	EST.					
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Title: WashU-Merck EST Project 1997		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
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Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA429945.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2113244		
RESULTS	10					
Qy	AA429945	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429945	AA429945				
DEFINITION	zwf10.s1 Soares_testis_NHT	Homo sapiens	cDNA clone	IMAGE:781291		
AUTHORS	Soares, M., Bowles, L., Duboue, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.					
VERSION	AA429945.1	GR:2113244				
KEYWORDS	EST.					
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Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Journal: Unpublished (1997)		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Organism: Homo sapiens		
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuLeProGluThrThrValGlyLysLeuLeu	80	Reference: AA429945		
Qy	176	GAATCTGTCGACCGCAGTAGCTGCTGCGCGGGCCCTTATTACCGGAGCTCTG	117	Definition: mRNA sequence.		
Qy	81	PhoAsnProSerGlyProTyroGlnLysLysProValHisGluLysLysGluValLeu	99	Accession: AA429945.1		
Qy	116	TTCATCCAGGGCTCTTACCGAGAAAGCCCTGTCATGAAAAGAGAGTTG	60	Version: GR:2113244		

and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "ORIGIN

BASE COUNT
119 a
101 c
92 g
120 t

Alignment scores:
Pred. No.: 4.8e-59 Length: 432
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AA429945 (1-432)

QY 1 MetAspAsnValGlnProIleTlySlysArgProPheCyspheSerVallysGlyHis 20
Db 361 ATGGATAACGCCAGCGAACATAAACATGCCCTTCGCTTAGTGAAAGCCAC 302
QY 21 VallysMetLeuValargLeuAspIleAspIleLeuSerIleLeuValThrValThrValheMetLeuIle 40
Db 301 GTGAAGAGCTGCGGCTGCAATTACACTCACACTCACAGTATCATGCATC 242
QY 41 ValSerValLeuIleLeuIleProGluThrThrLeuThrValGlyGlyGlyValPhe 60
Db 241 GTATCAGTGTTGGACTGATACAGAACACAACTGACAGTGTGAGGGTGT 182
QY 61 AlaLeuValThrAlaValCysCysIleuAlaAspGlyAlaLeuIleTyrArgLysLeuIle 80
Db 181 GCACITGTCAGCAGCTATGCTGTTGCGACGGGCCCTTACCGAAGCTCTG 122
QY 81 PheAsnProSerGlyProTyrglyllysProValHisGluIlysGluValLeu 99
Db 121 TTCAATCCACGGGTCTTACAGAAAAGCCTGTCATGAAAGAAAGAAGTTTG 65
RESULT 11

AI078580/c
LC/CUS AI078580
DEFINITION 452 bp mRNA linear EST 10-AUG-1998

ACCESSION 3'_mRNA sequence.
VERSION AI078580.1
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 452)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40m13 fwd. ER from Amersham

High quality sequence stop: 410.

Location/Qualifiers

1. .452

FEATURES source

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/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles

were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of T.M.A.G.E. clones 26032-265223,

BASE COUNT
125 a
110 c
97 g
120 t

ORIGIN
340480-345479, and 484480-489479."

Alignment scores:
Pred. No.: 5.12e-59 Length: 452
Score: 508.00 Matches: 99
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AI078580 (1-452)

QY 1 MetAspAsnValGlnProIleTlySlysArgProPheCyspheSerVallysGlyHis 20
Db 359 ATGGATAAGGTGCGGCCGAAATTAACATGCCTCTCTGCTACTGTGAAAGCCAC 300
QY 21 VallysMetLeuValargLeuAspIleLeuSerIleLeuValThrValThrValheMetLeuIle 40
Db 299 GTGAGATGCTGGCGCTGGATATATCACTCACTGTTACACAGTATTCATGCATC 240
QY 41 ValSerValLeuIleLeuIleProGluThrThrLeuThrValGlyGlyGlyValPhe 60
Db 239 GTACCTGTTGGACTATACAGAACACACACTGACAGTGTGAGGGGGTT 180
QY 61 AlaLeuValThrAlaValCysCysIleuAlaAspGlyAlaLeuIleTyrArgLysLeuIle 80
Db 179 GCACITGTCAGCAGCTATGCTGCTGCTGCGACGGGCCCTTACCGGAGCTCTG 120
QY 81 PheAsnProSerGlyProTyrglyllysProValHisGluIlysGluValLeu 99
Db 119 TTCAATCCCCAGGGTCTTACCAAGAAAAGCCCTGTCATGAAAGAAAGAAGTTTG 63
RESULT 12

AI743235/c
LOCUS AI743235
DEFINITION wg90a02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
ACCESSION IMAGE:237230 3'_mRNA sequence.
VERSION AI743235.1
KEYWORDS GI:5111523
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 453)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 378 Std Error: 0.00
Seq primer: -400P from Gibco.

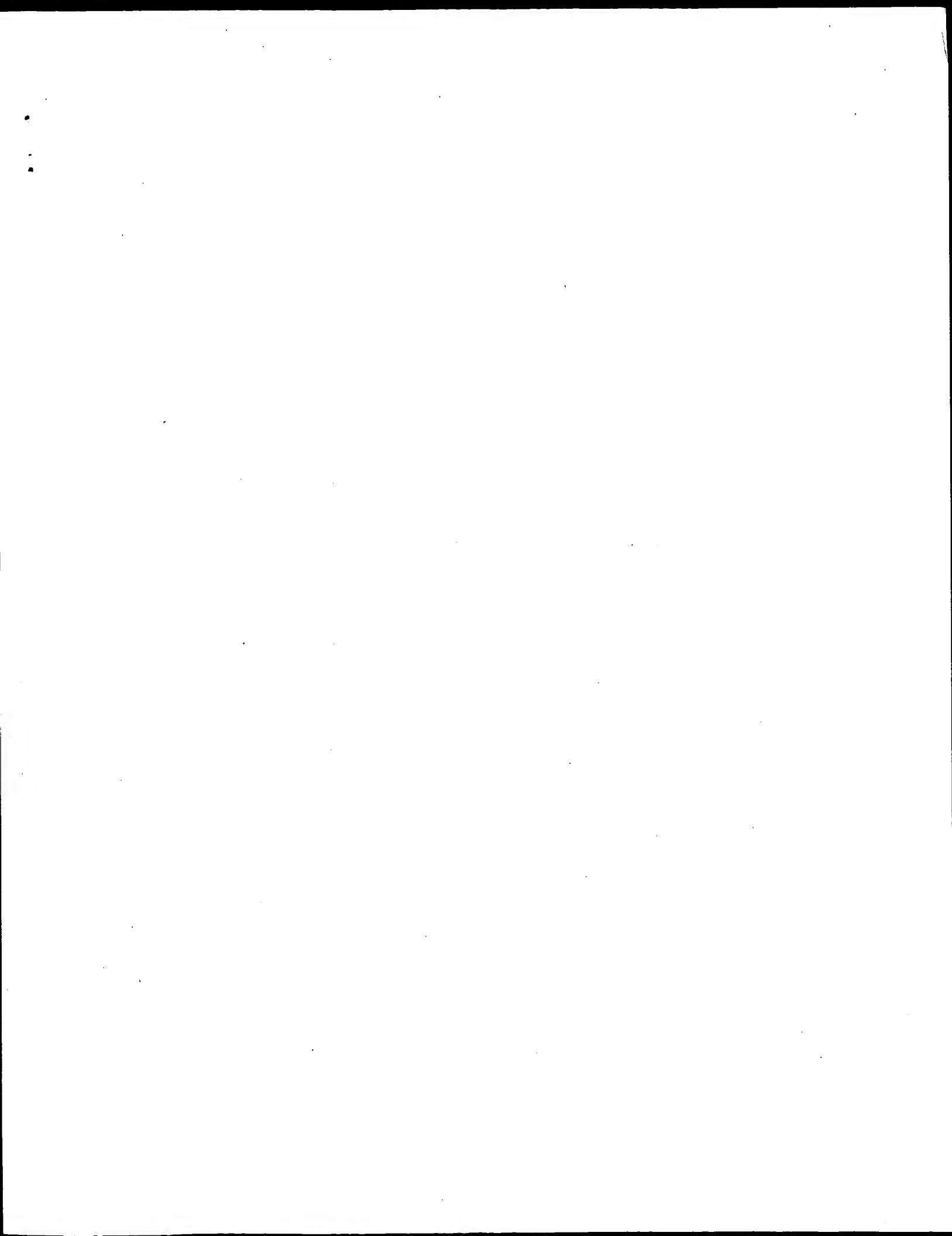
Location/Qualifiers

1. .453

FEATURES source

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/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.

FEATURES	source	<p>The sequence contained an oligo-dT track that was present in the strand cDNA and therefore this may represent a bona fide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)</p> <p>Seq primer: M13 Forward POLYA-Yes.</p> <p>Location/Qualifiers</p> <ol style="list-style-type: none"> 1. . . 510 <p>/organism="Rattus norvegicus" /strain="Sprague-Dawley" /db_xref="taxon:10116" /clone="UI-R-CAL-bjb-b-12-0-UI" /clone_1b="UI-R-CAL" /lab_host="DNI0B (Life Technologies)" /note="vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAL library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our website at rattus.ultra.genomics.org/. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996), TAG_SEQ=None found"</p>																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
FEATURES	source	<p>Location/Qualifiers</p> <ol style="list-style-type: none"> 1. . . 524 <p>/organism="Homo sapiens" /db_xref="taxon:9006" /clone="IMAGE:4820568" /clone_lid="NIM_MGC_95" /tissue_type="hippocampus" /lab_host="DNI0B" /note="organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI (gtcgacc); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NICRI, National Institute of Health). Note: this is a NIM_MGC Library."</p>																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
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BASE COUNT	ORIGIN	<p>US-09-801-115B-2 (1-99) x BG399486 (1-510)</p> <p>Alignment Scores:</p> <table border="1"> <thead> <tr> <th>Pred. No.:</th> <th>Score:</th> <th>Length:</th> <th>Matches:</th> <th>Conservative:</th> <th>Mismatches:</th> <th>Indels:</th> <th>Gaps:</th> </tr> </thead> <tbody> <tr> <td>508 00</td> <td>100 00%</td> <td>510</td> <td>99</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> </tr> <tr> <td>100 00%</td> <td>100 00%</td> <td>510</td> <td>99</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> </tr> <tr> <td>100 00%</td> <td>100 00%</td> <td>510</td> <td>99</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> </tr> <tr> <td>12</td> <td>12</td> <td>510</td> <td>99</td> <td>0</td> <td>0</td> <td>0</td> <td>0</td> </tr> </tbody> </table> <p>BASE COUNT</p> <p>US-09-801-115B-2 (1-99) x BG705303 (1-524)</p> <p>Alignment Scores:</p> <table border="1"> <thead> <tr> <th>Pred. 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GenCore version 5.1.6
copyright (c) 1993 - 2003 Compugen Ltd.

ON protein - nucleic search, using frame_plus_p2n model.

Run on: June 25, 2003, 11:54:40 ; Search time 215 Seconds
(without alignments)
1036.967 Million cell updates/sec

Title: US-09-801-115B-2
Perfect score: 508
Sequence: 1 MNVNQPKIKHRPFCCFSVKGH.....LFNPSPGPyQKRPVHKEVL 99

Scoring table: BLOSUM62

Xgapext	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370473

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL="frame+ p2n .model -DEV=xLP
-Q-/con2_1/USP0_spool/_USP090115/runat_20052003_141102_13574/app_query.fasta_1.263
-DB=N_Geneseq_101002 -QFM=fasta
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=Blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE_PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT_PTO -NORMEXT -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0901115 @CGNL_1_396 @runat_20062003_141102_13575 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESEQS=0 -WAIT -DBPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :

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N_Geneseq_101002;*
1: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1985.DAT:*
7: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1986.DAT:*
8: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1987.DAT:*
9: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1988.DAT:*
10: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1989.DAT:*
11: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1990.DAT:*
12: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1991.DAT:*
13: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1992.DAT:*
14: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1993.DAT:*
15: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1994.DAT:*
16: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1995.DAT:*
17: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1996.DAT:*
18: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1997.DAT:*
19: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1998.DAT:*
20: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1999.DAT:*
21: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2002.DAT:*
```

RESULT 1

ID	AAX97873	standard	cDNA	413 BP.
XX				
AC	AAX97873;			
XX				
DT	23-SEP-1999	(first entry)		

Human secreted protein encoding cDNA #61.

SECRETED PROTEIN HUMAN CDS

KW diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
KW diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
KW Human immune/haema
KW Human immune/haema
KW Human immune/haema

ALIGMENTS

OS Homo sapiens.

PN W09925825-A2.

PD 27-MAY-1999.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX
PF 13 - NOV-1998; 98WO-1B01862.
XX KW
PR 04 - SEP-1998; 98US-0099273.
XX KW
PR 13 - NOV-1997; 97US-0066677.
XX OS
PR 17 - DEC-1997; 97US-0069957.
XX PN
PR 09 - FEB-1998; 98US-0074121.
XX PN
PR 13 - APR-1998; 98US-0081563.
XX PD
PR 10 - AUG-1998; 98US-0096116.
XX PA
(GEST) GENSET.
XX PR
PR Bouquelaret L, Duclert A, Dumas Milne Edwards J;
PS XX DR
PS XX DR
PS XX P-PSDB; AAY36189.
PS XX
PS Extended cDNAs encoding secreted proteins
PS XX
PS Claim 1; Page 261; 307pp; English.
CC AX97813-x07906 represent extended cDNA's which encode novel human
CC thrombotic and osteopathic activity. The extended cDNAs can be used to
CC express secreted proteins or parts of them or to obtain antibodies
CC capable of binding to the secreted proteins. They may also be used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC Uses also include design of expression vectors and secretion vectors.
XX SQ sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;
Alignment Scores:
Pred. No.: 7.04e-58 Length: 413
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 20
Indels: 0
Gaps: 0
US-09-801-115B-2 (1-99) x AAX97873 (1-413)
QY 1 MetAspAsnValGlnProLysIleThrLysIleArgProPheCysPheservallyslyHis 20
DB 46 ATGGATACCGAGCGCAAGAAATAAACATCGCCCTTCAGTCAGTGTGAAAGGCCAC 105
QY 21 ValLysMetLeuArgLeuAspIleAsnSerLeuValThrValPheMetLeuIle 40
DB 106 GTGAGAGATGCGCGCGCTGATATTACACTCACGTTACAACAGTATCATCTC 165
QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyIglyValPhe 60
DB 166 GTATCTGTGTTGACTGATACAGAACCCACAGTTGAGCTTGAGGGGTGTT 225
QY 61 AlaLeuValThrAlaValCysCysLeuIaAspGlyValLeuIleTyrArgLysLeuLeu 80
DB 226 GCACTGTGAGCACTGATCTGCGCTGAGCAGGCCCTATMTCACCGGAAGCTCTCG 285
QY 81 PheAspProSerGlyProTrpGlnLysIleProValHISLysGluValLeu 99
DB 286 TTCAATGCCAGCGGCTTACCGAAAAGCTGATGATGAAAGAAGTTG 342
RESULT 2
ID ABK36006 standard; cDNA; 439 BP.
AC AC
AC ABK36006;
XX DT
XX DE
XX
XX Human secreted protein; hyperproliferative disorder; blood disorder; inflammatory disorder; immune deficiency disorder; blood disorder; autoimmune disorder;

XX KW
infectious disorder; allergic condition; neurodegenerative disorder;
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
XX OS
Home sapiens.
XX PN
WO20017289-A2.
XX XX
18-OCT-2001.
XX XX
29-MAR-2001; 2001WO-US10232.
XX PF
XX PR
06-APR-2000; 2000US-195605P.
XX XX
PA (GENE) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C, Wong GG;
PI Merberg D, Tracy M, Agostino MJ, Bowman MR, Spaulding V, Graham JR;
PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
DR XX
WPI: 2002-179322/23.
PS XX
PS Claim 1; Page 296-297; 393pp; English.
CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g., cancer), immune deficiency disorders (e.g., severe combined
CC immunodeficiency, SCID), autoimmune disorders (e.g., multiple
CC sclerosis), blood disorders (e.g., thrombocytopenia), inflammatory
CC disorders (e.g., arthritis), infectious disorders (e.g., hepatitis),
CC Alzheimer's disease), liver fibrosis, neurodegenerative disorders (e.g.,
CC haemophilia), and tumours. The polynucleotide sequences of the
CC invention are also useful in gene therapy. ABK35610-ABK36232 represent
CC the cDNA sequences of the invention that encode for novel human
secreted proteins.
XX SQ Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;
Alignment Scores:
Pred. No.: 7.64e-58 Length: 439
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 24
Indels: 0
Gaps: 0
US-09-801-115B-2 (1-99) x ABK36006 (1-439)
QY 1 MetAspAsnValGlnProLysIleThrLysIleArgProPheCysPheservallyslyHis 20
DB 81 ATGGATAACGTGCAGCGCAAGAAATAAACATCGCCCTTCAGTCAGTGTGAAAGGCCAC 140
QY 21 ValLysMetLeuArgLeuAspIleAsnSerLeuValThrValPheMetLeuIle 40
DB 141 GTGAGAGATGCTGGCGCGATATTACACTCACGTTACAACAGTATCATCTC 200
QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyIglyValPhe 60
DB 201 GATCCTGTGTTGACATGATACAGAACACATGAGCTGTTGAGCTGAGGGGTGTT 260
QY 61 AlaLeuValThrAlaValCysCysLeuIaAspGlyIglyValLeuIleTyrArgLysLeu 80

PS Claim 1: Page 320: 721pp; English.

XX
 CC This sequence represents a nucleic acid molecule designated Gene 88 from
 CC the human cDNA clone HAUAV32 (deposited as clone ATCC 97901 and ATCC
 CC 2047) which encodes a secreted human protein. The gene can be used to
 CC generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 166 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-#9812; amino acid sequences AWW7431-WI5026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological conditions
 CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new
 CC polynucleotides. Specific uses are described for each of the 186
 CC (see AAV59511 for described uses).

XX Sequence 504 BP; 143 A; 105 C; 128 G; 127 T; 0 other;

SQ Alignment Scores:

Pred. No. :	9.22e-58	Length:	504
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:		Gaps:	19

US-09-801-115B-2 (1-99) x AAV59598 (1-504)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProHeCysPheSerVallysGlyHis 20
 ||||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 131 ATGGATAACGTGTCAGCCGAATAAACATGCCCTCTGCTCTGAAAGGCCAC 190
 QY 21 ValLySmetLeArgLeuAspIleLeasnSerLeuValThrRhrValPhemeteLeuile 40
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 191 GTGAAAGATGCTGGGCGTGATATTACTACTGTAACACAGTATCATGCATC 250
 QY 41 ValSerValLeuLeuIleProGlutThrThrLeuThrValGlyGlyValPhe 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 251 GATCTCGTGTTGCACTGATACCAGAACACATGACAGTGTTGGAGGGTT 310
 QY 61 AlaLeuValThrAlaValCysCysLeuLeuAspGlyAlaLeuLeuIlePheArgLysLeu 80
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 311 GCACTTGACAGCAGTGCTGCTGCCGACGGGCCCTATTACCGAAGCTTCG 370
 QY 81 PheAsnProSerGlyProTyroGlnLysLysProValHisGluLysGluValLeu 99
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 371 TCAATCCCAGGGCTCTTACCGAAAAASCCTGTGCAAGAAAAAGAGTTTG 427
 RESULT 4
 AAV59746
 ID AAV59746 standard; DNA; 506 BP.
 XX
 AC AAV59746;
 XX DT 19-JAN-1999 (first entry)
 DE Human secreted protein gene 88 clone HAUAV32.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 OS Homo sapiens.
 XX
 PN WO9839448-A2.

XX PD 11-SEP-1998.
 XX PF 06-MAR-1998; 98WO-US04493.
 XX PR 02-OCT-1997; 97US-0061060.
 XX PR 07-MAR-1997; 97US-0036621.
 XX PR 07-MAR-1997; 97US-0041611.
 XX PR 07-MAR-1997; 97US-004162.
 XX PR 07-MAR-1997; 97US-004163.
 XX PR 07-MAR-1997; 97US-0041333.
 XX PR 07-MAR-1997; 97US-0041334.
 XX PR 07-MAR-1997; 97US-0040336.
 XX PR 07-MAR-1997; 97US-0041626.
 XX PR 11-APR-1997; 97US-0043111.
 XX PR 11-APR-1997; 97US-0043312.
 XX PR 11-APR-1997; 97US-0043313.
 XX PR 11-APR-1997; 97US-0043314.
 XX PR 11-APR-1997; 97US-0043568.
 XX PR 11-APR-1997; 97US-0043569.
 XX PR 11-APR-1997; 97US-0043576.
 XX PR 11-APR-1997; 97US-0043578.
 XX PR 11-APR-1997; 97US-0043669.
 XX PR 11-APR-1997; 97US-0043670.
 XX PR 11-APR-1997; 97US-0043671.
 XX PR 11-APR-1997; 97US-0043672.
 XX PR 11-APR-1997; 97US-0043674.
 XX PR 23-MAY-1997; 97US-0047492.
 XX PR 23-MAY-1997; 97US-0047500.
 XX PR 23-MAY-1997; 97US-0047502.
 XX PR 23-MAY-1997; 97US-0047503.
 XX PR 23-MAY-1997; 97US-0047581.
 XX PR 23-MAY-1997; 97US-0047582.
 XX PR 23-MAY-1997; 97US-0047583.
 XX PR 23-MAY-1997; 97US-0047584.
 XX PR 23-MAY-1997; 97US-0047585.
 XX PR 23-MAY-1997; 97US-0047586.
 XX PR 23-MAY-1997; 97US-0047587.
 XX PR 23-MAY-1997; 97US-0047588.
 XX PR 23-MAY-1997; 97US-0047589.
 XX PR 23-MAY-1997; 97US-0047590.
 XX PR 23-MAY-1997; 97US-0047592.
 XX PR 23-MAY-1997; 97US-0047593.
 XX PR 23-MAY-1997; 97US-0047594.
 XX PR 23-MAY-1997; 97US-0047595.
 XX PR 23-MAY-1997; 97US-0047596.
 XX PR 23-MAY-1997; 97US-0047597.
 XX PR 23-MAY-1997; 97US-0047598.
 XX PR 23-MAY-1997; 97US-0047600.
 XX PR 23-MAY-1997; 97US-0047601.
 XX PR 23-MAY-1997; 97US-0047612.
 XX PR 23-MAY-1997; 97US-0047613.
 XX PR 23-MAY-1997; 97US-0047614.
 XX PR 06-JUN-1997; 97US-0047615.
 XX PR 23-MAY-1997; 97US-0047617.
 XX PR 23-MAY-1997; 97US-0047618.
 XX PR 23-MAY-1997; 97US-0047632.
 XX PR 23-MAY-1997; 97US-0047633.
 XX PR 23-MAY-1997; 97US-0047634.
 XX PR 13-JUN-1997; 97US-0049610.
 XX PR 08-JUL-1997; 97US-0051926.
 XX PR 16-JUL-1997; 97US-0052874.
 XX PR 18-AUG-1997; 97US-0053724.
 XX PR 22-AUG-1997; 97US-0056630.
 XX PR 22-AUG-1997; 97US-0056631.
 XX PR 22-AUG-1997; 97US-0056632.
 XX PR 22-AUG-1997; 97US-0056633.
 XX PR 22-AUG-1997; 97US-0056637.
 XX PR 22-AUG-1997; 97US-0056662.

PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056872.
 PR 22-AUG-1997; 97US-0056874.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056890.
 PR 22-AUG-1997; 97US-0056891.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056895.
 PR 22-AUG-1997; 97US-0056900.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057669.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PT Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX WPI: 1998-506364/43.
 DR P-PSDB; AHW74951.
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1; Page 472; 721pp; English.
 XX
 CC This sequence represents a nucleic acid molecule designated Gene 88 from
 CC the human cDNA clone HAUWV3 (deposited as clone ATCC 9987 and ATCC
 CC 209043) which encodes a secreted human protein. The gene can be used to
 CC generate fusion proteins by linking the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).
 XX
 SQ sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;
 Alignment Scores:
 Pred. No.: 9 27e-58 Length: 506
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 19 Indels: 0
 Gaps: 0
 DB:
 US-09-801-115B-2 (1-99) x AAV59746 (1-506)
 QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIysGlyHis 20
 Db 117 ATGGATACGGTGCAGCCAAATAAACATCCGCCCTCTGCTTCAGTGTAAGGCCAC 176
 QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuile 40
 Db 177 GTGAGAAGCTGGGGCGGAGTATTCACACTGCTAACACATPATTCATGCAC 236
 QY 41 ValSerValLeuIlaLeuIleProGluIhrThrThrLeuThrValGlyGlyGlyValPhe 60
																								Bouquerelret I, Dumas J, Duclert A;																																							
 XX WPI: 2000-442637/38.
 DR P-RSDB; AAB25768.
 XX
 PT Polynucleotides and polypeptides encoding proteins with signal
 PT peptides, useful in diagnostic, forensic, gene therapy and chromosome
 PT mapping procedures -
 XX
 PS Claim 1; Page 169-170; 306pp; English.
 XX
 CC This sequence represents human cDNA encoding a secreted protein. The
 CC invention relates to sequences AAV87725-8774 which encode human
 CC secreted proteins AAB5763-B25812. The proteins include signal peptides.
 CC Included in the invention are a host cell containing one of the cDNA
 CC sequences, and a purified antibody capable of binding to one of the
 CC secreted proteins. Also contained in the invention are methods for
 CC storing the sequence data on a computer system, and a method for
 identifying features of the cDNA sequences using a computer programme.

CC The cDNAs are useful for expressing secreted proteins or fragments to
 CC obtain antibodies capable of specifically binding to the secreted
 CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene
 CC therapy and chromosome mapping procedures and may be used to design
 expression vectors and secretion vectors. The proteins of the invention
 may be used to treat diseases including cancer, autoimmune diseases/
 cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
 disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
 disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis,
 neurodegenerative disorders, graft rejection, Alzheimer's disease,
 dementia, hyperlipidaemia, septic shock and impotence.

XX SQ Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Alignment scores:

Pred. No.: 9.49e-58 Length: 515
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-801-115B-2 (1-99) x AAA87730 (1-515)

QY 1 MetAspAsnValGlnProLysIleVshisArgPheProCysPheSerValGlyHis 20
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 144 ATGATACAGTCGAGCCAAATAAACATGCCCTCTGCTTCGTGTGAAAGCCAC 203
 QY 21 ValIysMetLeuArgLeuAspIleLeasnSerIleValThrIhrValPheMetLeuIle 40
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 204 GTGAGAAGACTGGCGCNGATATATCACACTACTGTAACACAGTATCATGCATC 263
 QY 41 ValSerValLeuAlaIleUleProGluIhrThrLeuThrValGlyGlyValPhe 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 264 GTATCTGTTGGCCTGACTGATACCAAGAACACACATGACAGTTGGGGGGTT 323
 QY 61 AlaLeuValIhrValAlaValCysCysLeuAlaAspGlyAlaLeuIleThrArgLysLeuIle 80
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 324 GCACCTGTGACAGCAGTATGCTGCTGCGGAGGCGCTATTACCGGAACITCTG 383
 QY 81 PheAsnProSerGlyProtryGlnLysLysProvalIhsGluLysLysGluValIle 99
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 384 TTCAATCCCAGGGCTTACAGAAANAGCCGTCGATGAAANAAAAGAGTTTG 440

RESULT 6
 AAF64012
 ID AAF64012 standard; cDNA; 515 BP.

XX

AC AAF64012;

XX

AC

PT Chemotaxic factor useful for treatment and diagnosis of immunocyte disorders - has immunocyte chemotactic stimulating factor

PR 15-SEP-2000; 2000US-0663870.

PT XX (HYSE-) HYSEQ INC.

PA XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PS XX DR Cao Y, Drmanac RA, Zhang J, Wernham T;

XX DR WPI; 2001-476164/51.

XX PR-PDB; AAM23856.

CC Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -

CC PR XX PS XX Claim 1; Page 451; 1275pp; English.

CC The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.

SQ Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;

Alignment Scores: Pred. No.: 9.97e-58 Length: 534 Score: 508.00 Matches: 99 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 21 Gaps: 0

US-09-801-115B-2 (1-99) x AAA38006 (1-534)

Qy 1 MetAPsAvalGlnProLysIleYsHsArgProPheCysPheSerValLysGlyHis 20

Db 152 ATGGATGACGCGCAGCAAAATAAACACGCCCTTGTCAGTGAGAAGGCCAC 211

Qy 21 ValIysMetLeuArgLeuAspIleLeasnSerLeuValThrThrValpHeMetLeuIle 40

Db 212 GTGAAGATGCAGCGGCGTGTATTACCGAAAGCTGATCAGTACGTAAGTCATCarc 271

Qy 41 ValSerValLeuAlaLeuIleProGlutThrThrLeuThrValGlyGlyIleValPhe 60

Db 272 GTATCTGTGTTGACTGATCCAGAACACAGATGACAGTGGTSGAGGGCTGTT 331

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyIleAlaLeuIleTyrglyLeuLeu 80

Db 332 GCATCTGTGAGAGCACTGATGCTGCGACGGGCCCTATTACCGAAAGCTCTG 391

Qy 81 PheAsnProSerGlyProTyrglyIysProvalHisGluIysGluValLeu 99

Db 392 TTCAATCCCAGGGTCTTACCGAAAAAGCCTGTCATGAAAAAAAGAGTrrTGTG 448

RESULT 8 ARH9815/C ID AAH98515 standard; cDNA; 538 BP.

XX AC AAH98515;

XX DT 12-OCT-2001 (first entry)

DE Human EST-derived coding sequence SEQ ID NO: 372.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.

KW Homo sapiens.

XX WO200154477-A2.

XX DE 02-AUG-2001.

XX PR 25-JAN-2001; 2001WO-US02687.

XX PR 25-JAN-2000; 2000US-0491404.

XX PR 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.

SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

Alignment Scores: Pred. No.: 1.01e-57 Length: 538 Score: 505.00 Matches: 99 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Indels: 0 DB: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAH98515 (1-538)

Qy 1 MetAPsAvalGlnProLysIleYsHsArgProPheCysPheSerValLysGlyHis 20

Db 366 ATGGATAAGTGGCACGCCAAATAAACATGCGCCCTTGCTCTGCTGAGGCCAC 307

Qy 21 ValIysMetLeuArgLeuAspIleLeasnSerLeuValThrThrValpHeMetLeuIle 40

Db 306 GTGAGATGCTGGCGCTGGATATATCACTCACTGGTAACTACAGTATGAGTCATC 247

Qy 41 ValSerValLeuAlaLeuIleProGlutThrThrLeuThrValGlyGlyIleValPhe 60

Db 246 GTATCTGTGCGCACTGATACCAAGAACCCACACTGACAGTTGGAGGGCTGTT 187

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyIleAluIleTyrglyLeuLeu 80

Db 186 GCATCTGTGAGAGCACTGATGCTGCTCCGACGGGCCCTATTACCGAAAGCTG 127

Qy 81 PheAsnProSerGlyProTyrglyIysProvalHisGluIysGluValLeu 99

Db 126 TTCAATCCCAGGGTCTTACCGAAAAAGCCTGTCATGAAAAGAGAGTITG 70

RESULT 9 AAH98548/C ID AAH98548 standard; cDNA; 538 BP.

XX AC AAH98548;

XX DT 12-OCT-2001 (first entry)

DE Human EST-derived coding sequence SEQ ID NO: 405.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.

KW Homo sapiens.

PN WO20015477-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US02687.
 XX
 PR 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617745.
 PR 15-SEP-2000; 2000US-0663870.
 XX
 PA (HYSEQ-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX WPI; 2001-476164/51.
 DR P-PSDB; AAM23889.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX
 PS Claim 1; Page 467; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention.
 SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.01e-57 Length: 538
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-801-115B-2 (1-99) x AAH98548 (1-538)
 QY 1 MetAspAsnValGlnProLysIleLysArgProPhiCysPheSerVallysGlyHis 20
 DB 366 ATGGATAACGTGCGAGCCAAATAAACATGCCCTTCAGTGIGAAAGCCAC 307
 QY 21 ValIysMetLeuArgLeuAspIleAspIleAsnSerLeuValThrThrValPheMetLeuIle 40
 DB 306 GIGAGATGTCGGGCCTGAGATATGACTACTGTTAACACAGTATCATGCATC 247
 QY 41 ValSerValLeuAlaLeuIleLeuProGluThrThrLeuThrValGlyGlyValPhe 60
 DB 246 GTACCTGGTTGCAAGATACCAAGAAACCACACATGAGCTGTTGGAGGGGTT 187
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyYalaLeuIleLeuTyrArgLysLeu 80
 DB 186 GCACTGGAGCACAGCAGTAGCTGCTGGCCAGGGGCCCTATTACCGAAGCTCG 127
 QY 81 PheAsnProSerGlyProTyroGlnLysLysProValHisGluLysGluValLeu 99
 DB 126 TCAATCCAGGGTCTTACCAAGAAAAGCTGTGCAATGAAAAAAGAGTTG 70
 RESULT 10
 AH34835 ID AAH34835 standard; cDNA; 558 BP.
 XX AAH34835;
 XX DT 03-SEP-2001 (first entry)
 XX

DE Human colon cancer antigen encoding cDNA SEQ ID NO:1917.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; ss.
 XX
 OS Homo sapiens.
 XX
 PR 28-SEP-2000; 2000WO-US26524.
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-016280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 DR WPI; 2001-235357/24.
 DR P-PSDB; AAG75130.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 1; Page 3428; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression or deletions in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SO Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;
 Alignment Scores:
 Pred. No.: 1.00e-57 Length: 558
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-801-115B-2 (1-99) x AAH34835 (1-558)
 QY 1 MetAspAsnValGlnProLysIleLysArgProPhiCysPheSerVallysGlyHis 20
 DB 147 ATGGATAACGTGCGAGCCAAATAAACATGCCCTTCAGCTGAAAGCCAC 206
 QY 21 ValIysMetLeuArgLeuAspIleAspIleAsnSerLeuValThrThrValPheMetLeuIle 40
 DB 207 GTAGAGATGCTGGCGCTGGATATCAGCTACGTTAACACAGTATCATGCATC 266
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPhe 60
 DB 267 GTATCTGGTGGCAGTACCAAGAAACCACACATGAGCTGTTGGAGGGGTT 326
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyYalaLeuIleLeuTyrArgLysLeu 80

Db 327 GCACITGTCAGCAGTAGTCTGCTTGCCAGCGGGCCTTAATTACCGGAAGCTTCCTG 386
 CC |||||||
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 QY 81 PheAsnProSerGlyProtryGlnLyslSsProValHisGluLysLysGluValLeu 99
 CC |||||||
 Db 387 TTCAATCCACGCGGCCTTACAGAAAGCCCTGCGTGAAGAAAAGAAGTTG 443
 CC |||||||
 RESULT 11
 AAS4932
 ID AAS4932 standard; cDNA: 655 BP.
 XX
 AC AAS4932;
 XX 18-DEC-2001 (first entry)
 DE cDNA encoding novel human secretory protein, Seq ID No 13.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia reperfusion injury; haemopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen; ss.
 KW
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0663363.
 PR 20-OCT-2000; 2000US-0693267.
 PR
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PT Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang Ji;
 XX
 DR WPI: 2001-589934/66.
 DR
 DR P-PSDB; AU28032.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Claim 1; SEQ ID No 13; 107P; English.
 XX
 The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haemopoiesis, stem cell survival, bone growth
 CC and remodelling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haemopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 XX
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorder e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS4920-AAS15295 represent novel human secreted protein
 CC coding sequences of the invention.
 XX Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;
 SQ Alignment Scores:
 Pred. No.: 1 MetAspAsnValGlnProLysIleLysIleArgProHeaCysPheSerValLeuGlyHis 20
 QY |||||||
 Db 134 ATGGATAACGTGAGCCGAATAAACATGCCCTCTGTCAGTGTGAGGCCAC 193
 QY |||||||
 Db 21 ValIysMetLeuargLeuAspIleAspIleIeasnserLeuvalThrIleValPheMetLeuile 40
 QY |||||||
 Db 194 GTGAGATACTGCGCTGGATATTCACACTACACTACACTACAGTGTACACAATTCATGCGCATC 253
 QY 41 valSerValLeuIleLeuIleProGluThrThrIleIleValGlyIgylValPhe 60
 QY |||||||
 Db 254 GTATCTGTCGGCATCTGATACCAAGAACACCACACTATGACAGTTCGGGGAGGGTTT 313
 QY 61 AlaLeuValThrIleValCysCysLeuIalaAspGlyAlaLeuIleIleValGlyLeuLeu 80
 QY |||||||
 Db 314 GCACITGTCAGCAGTAGTCTGCTTGCCAGCGGGCCTTAATTACCGGAAGCTTCCTG 373
 QY 81 PheAsnProSerGlyProtryGlnLyslSsProValHisGluLysLysGluValLeu 99
 DB 374 TTCAATCCACGCGGCCTTACAGAAAGCCCTGCGTGAAGAAAAGAAGTTG 430
 RESULT 12
 ID AAA15919
 ID AAA15919 standard; cDNA; 297 BP.
 XX
 AC AAA15919;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 Human protein clone HP10357 coding sequence.
 XX
 KW Human protein; hydrophobic domain; nutritional source; haemopoiesis;
 KW cytokine production; cell proliferation; cell differentiation;
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; liver fibrosis; reperfusion injury;
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
 KW coagulation disorder; myocardial infarction; inflammatory condition;
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
 KW nephritis; therapy; ss.
 XX
 OS Homo sapiens.

PW 0020005367-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 22-JUL-1999; 99WO-JP03929.
 XX
 PR 24-JUL-1998; 98JP-0208820.
 PR 07-AUG-1998; 98JP-0224105.
 PR 25-AUG-1998; 98JP-0238116.
 PR 09-SEP-1998; 98JP-0254736.
 PR 29-SEP-1998; 98JP-0275505.
 XX
 PA (SAGA) SAGAMI CHEM RES CENT.
 PT (PROT-) PROTEGENE INC.
 XX
 PI Kato S.; Kimura T.;
 XX
 DR WPI; 2000-182694/16.
 XX
 P-PADB; AAY94861.
 XX
 PT Novel human proteins having hydrophobic domains useful for treating
 PR osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
 multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
 XX
 PG Claim 3; Page 217-218; 351pp; English.
 XX
 CC This sequence encodes a human protein of the invention, which has
 hydrophobic domains. The DNA sequences can be used as a probe or as a
 genetic marker. The protein can also be used as a marker, and to identify
 potential genetic disorders. The DNA and protein can also be used as
 nutritional sources or supplements. The protein exhibits cytokine, cell
 proliferation, cell differentiation activities and induces production of
 other cytokines in certain cell populations. The protein also exhibits
 immune stimulating or immune suppressing activity. It can be used in the
 treatment of various immune deficiencies and disorders, and to treat
 infectious diseases caused by viral, bacterial, fungal or other
 infections. The protein is also used for treating autoimmune disorders
 such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
 arthritis. It is also useful in the treatment of allergic reactions and
 conditions such as asthma, and in immune suppression after organ
 transplantation. The protein is useful in regulation of hematopoiesis
 and consequently in the treatment of myeloid or lymphoid cell
 deficiencies. It is also used in compositions for tissue growth or
 regeneration. The protein is also used in the treatment of osteoporosis
 or osteoarthritis and in the treatment of periodontal disease and other
 tooth repair processes. The protein is used in the treatment of nervous
 system disorders such as Alzheimer's disease, Parkinson's disease, and
 Huntington's disease. They are useful for protection or regeneration and
 treatment of lung or liver fibrosis, reperfusion injury in various
 tissues, and conditions resulting from systemic cytokine damage. They are
 also used for promoting or inhibiting tissue differentiation. They are
 also used as contraceptives since they exhibit activin or inhibin related
 activities and as a fertility inducing therapeutic. They are used for
 treating various coagulation disorders and in treatment and prevention of
 conditions resulting from coagulation activities e.g. myocardial
 infarction or stroke. They also acts as receptors, receptor ligands or
 inhibitors or agonists of receptor/ligand interactions. They are used to
 treat inflammatory conditions such as septic shock, sepsis, ischaemia
 reperfusion injury, arthritis, and nephritis. They can be used to
 prevent tumours.
 XX
 SQ Sequence 297 BP; 81 A; 68 C; 72 G; 76 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 1.52e-57 Length: 297
 Score: 504.00 Matches: 98
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 98.99% Mismatches: 0
 Query Match: 99.21% Indels: 0
 DB: 21 Gaps: 0
 US-09-801-115B-2 (1-99) x AAA15919 (1-297)

QY 1 MetaspasnValGlnProlylsileylsIshisarProphesyPheSerVallysGlnHis 20
 YY 1 ATGGTTAACCTGCAGCCGAATAAACCTCGCCCTTGCTCAGTCAGTCAGTCACAGGCCAC 60
 Db 21 ValysMetleuargLeuaspIleileasnSerileuValthrThrvalPhenketleuile 40
 QY 61 GrGAGATGCTGCCGCGGATATTACACTCACTGGTACACAGTATTGCTCATC 120
 Db 41 ValservalleuAlaIeuleProgluThrThrIeuThrvalGlyGlyGlyValphe 60
 QY 121 GTATCTGCTGCTGGCACTGTGATACCAGAAACCACATGACACTTGCTGGAGGGTT 180
 Db 61 AlateuvalIthrAlaValcysCysLeuAlaAspGlyAlaLeutleTarglySteLeu 80
 Db 181 GCACCTGTCAGCAGCTGATGCTGCTTCCGAGGGCCCTTAATTACCGGAGCTCTG 240
 QY 81 PheasnProSerGlyProtryGlyInlyLysproValHsGluLysLysGluValleu 99
 Db 241 TTCAATCCCCAGGGTCTTACACAGCAAAGCCCTGCTGATGAAAGAAAAGAGTTTG 297
 RESULT 13
 XX
 AAIA15929 DT 12-JUN-2000 (first entry)
 ID AAIA15929 standard; cDNA; 467 BP.
 XX
 AC AAIA15929;
 XX
 DE Human protein clone HP10357 full length coding sequence.
 XX
 KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;
 KW cytokine production; cell proliferation; cell differentiation;
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
 KW coagulation disorder; myocardial infarction; inflammatory condition;
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
 KW nephritis; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200005367-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 22-JUL-1999; 99WO-JP03929.
 XX
 PR 24-JUL-1998; 98JP-0208820.
 PR 07-AUG-1998; 98JP-0224105.
 PR 25-AUG-1998; 98JP-0238116.
 PR 09-SEP-1998; 98JP-0254736.
 PR 29-SEP-1998; 98JP-0275505.
 XX
 PA (SAGA) SAGAMI CHEM RES CENT.
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 XX
 PI Kato S., Kimura T.;
 XX
 DR WPI; 2000-182694/16.
 XX
 P-PADB; AAY94861.
 XX
 PT Novel human proteins having hydrophobic domains useful for treating
 PR osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
 multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
 XX
 PS Claim 4; Page 228; 351pp; English.
 XX
 CC This sequence encodes a human protein of the invention, which has
 hydrophobic domains. The DNA sequences can be used as a probe or as a
 genetic marker. The protein can also be used as a marker, and to identify

CC potential genetic disorders. The DNA and protein can also be used as nutritional sources or supplements. The protein exhibits cytokine, cell proliferation, cell differentiation activities and induces production of other cytokines in certain cell populations. The protein also exhibits immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat infectious diseases caused by viral, bacterial, fungal or other infections. The protein is also used for treating autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid arthritis. It is also useful in the treatment of allergic reactions and conditions such as asthma, and in immune suppression after organ transplantation. The protein is useful in regulation of haematopoiesis and consequently in the treatment of myeloid or lymphoid cell deficiencies. It is also used in compositions for tissue growth or regeneration. The protein is also used in the treatment of osteoporosis or osteoarthritis and in the treatment of periodontal disease and other tooth repair processes. The protein is used in the treatment of nervous system disorders such as Alzheimer's disease, Parkinson's disease, and Huntington's disease. They are useful for protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. They are also used for promoting or inhibiting tissue differentiation. They are also used as contraceptives since they exhibit activin or inhibin related activities and as a fertility inducing therapeutic. They are used for treating various coagulation disorders and in treatment and prevention of infarction or stroke. They also acts as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. They are used to treat inflammatory conditions such as septic shock, sepsis, ischaemia reperfusion injury, arthritis, and nephritis. They can be used to prevent tumours.

XX Sequence 467 BP; 118 A; 101 C; 121 G; 127 T; 0 other;

SQ Alignment Scores:

Pred. No.:	2.81e-57	Length:	467
Score:	504.00	Matches:	98
Percent. Similarity:	100.00%	Conservative:	1
Best Local Similarity:	98.99%	Mismatches:	0
Query Match:	99.21%	Indels:	0
DB:	21	Gaps:	0

US-09-801-115B-2 (1-99) x AAA15929 (1-467)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20

Db 114 ATGGATACAGTGCGAGCGGAATAAACATGCCCTTCGCTCTGAGAAGGCCAC 173

Qy 21 ValLeuMetLeuArgLeuAspIleLeuAsnSerLeuValThrThrValPheMetLeuIle 40

Db 174 GTGAGAGGCTCGGGTGGATATTACACTCACTGTAQAAACAGTATCATGCATC 233

Qy 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyGlyValPh 60

Db 234 GATCTCTGTTGGCACAGTACCAAGAACACACAGTGACAGTTGGAGGGTGT 293

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80

Db 294 GCACTTGAGCAGCTATGCTCTGCGAGGGCCCTATTACCGAGGTTCTG 353

Qy 81 PheAspProSerGlyProTygGlyLysProValHisGluLysGluValLeu 99

Db 354 TTCATCCAGGGCTTACCGCAAAGCTGTCATGAAAGAAAAGAGTTG 410

RESULT 14

ID AX97826 standard; cDNA: 500 BP.

XX AX97826;

XX 23-SEP-1999 (first entry)

XX Human secreted protein encoding cDNA #14.

XX Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic; KW diagnostic; gene therapy; chromosome mapping; secretion vector; ss.

XX OS Homo sapiens.

XX PN WO9925825-A2.

XX PD 27-MAY-1999.

XX PR 13-NOV-1998; 98WO-1B01862.

XX PR 04-SEP-1998; 98US-0039273.

XX PR 13-NOV-1997; 97US-0056677.

XX PR 17-DEC-1997; 97US-0059957.

PR 09-FEB-1998; 98US-0074121.

PR 13-APR-1998; 98US-001563.

PR 10-AUG-1998; 98US-0056116.

XX PA (GEST) GENSET.

XX DR WPI; 1998-347472/29.

XX PT P-PDB; AAY36142.

XX PT Extended cDNAs encoding secreted proteins

XX PS Example 28; Page 173-174; 307pp; English.

XX CC AAX7813-X97906 represent extended cDNA's which encode novel human secreted proteins (see KAI36129 Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.

XX SQ Sequence 500 BP; 135 A; 102 C; 125 G; 129 T; 9 other;

SO Alignment Scores:

Pred. No.:	2.96e-55	Length:	500
Score:	489.00	Matches:	98
Percent. Similarity:	98.00%	Conservative:	0
Best Local Similarity:	98.00%	Mismatches:	1
Query Match:	96.26%	Indels:	1
DB:	20	Gaps:	0

US-09-801-115B-2 (1-99) x AAX97826 (1-500)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20

Db 132 ATGGATACGTCGAGCCGAATAAACATGCCCTTCGCTCTGCTCAGTGAAAGGCCAC 191

Qy 21 Val-LysMetLeuArgLeuAspIleLeuAsnSerLeuValThrThrValPheMetLeuIle 40

Db 192 GTGAGAGTCTGCGCTGATATACTGCTACAGTATCATGCATC 251

Qy 40 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPh 60

Db 252 CGTACTCTGTTGGCACTGATACCAAGAACACACAGTGACAGTTGGAGGGTGT 311

Qy 60 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80

Db 312 TGCACCTGAGCAGCACTGCTGCTGCGACGGGCCCTATTACCGAGGTTCT 371

Qy 80 upheasnProSerDlyProTygGlyLysProValHisGluLysGluValLeu 99

Db 372 GTTCATCCAGGGCTTACCGCAAAGCTGTCATGAAAGAAAAGAGTTG 429

RESULT 15

ID AAA38007 standard; cDNA: 459 BP.

XX
AC AAA38007:
XX
DT 22-AUG-2000 (first entry)
XX
DE UCK-2 nucleotide sequence.
XX
KW UCK-2; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;
KW radiotherapy; chemotherapy; human; ss.
XX
OS Homo sapiens.
PN CNI-244384-A.
XX
PR 14-MAY-1999; 99CN-0107284.
XX
PA (UVBE-) UNIV BEIJING MEDICAL.
XX
PI Ma, D.; Han, W.; Zhang, Y.;
XX
DR WPT; 2000-398170/34.
DR P-PSDB; AAY98143.

PT Chemotactic factor useful for treatment and diagnosis of immunocyte disorders - has immunocyte chemotactic stimulating factor

PS Example 4; Fig 2; 31pp; Chinese.

XX
CC This sequence represents an UCK-2 cDNA sequence encoding a chemotaxis factor polypeptide. The UCK-2 protein exhibits immunocyte chemotaxis activity and a haemopoiesis stimulating effect. The invention relates to UCK proteins, their encoding nucleotide sequences and antibodies and antagonists against the proteins. The nucleotide and protein sequences are useful for the preparation of a composition for the diagnosis and treatment of diseases associated with abnormal immunocyte function and low haemopoiesis function caused by radiotherapy and chemotherapy used to treat tumours and other diseases.

XX
SQ Sequence 459 BP; 123 A; 99 C; 96 G; 141 T; 0 other;

Alignment scores:
Pred. No.: 5.43e-53 Length: 459
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
DB: 21 Gaps: 1

US-09-801-115B-2 (1-99) x AAA38007 (1-459)

QY 1 MetaspasValGlnProLysIleLysIleArgProPheCysPheSerValLysGlyRis 20
1 ATGGATAAGTGCGGCCGAAATTAACACATGCCCTTCGCTTCAGTGTGAAGGCCAC 60
QY 21 VallysMetLeuIurg----- 25
DB 61 GTGAAAGATGCTGCGGCTGCACTAAGCTGACATCTATGACCTTTTATCATCGCAAA 120
QY 25 ----- 25
DB 121 GCCCCTGACCATAATTTGTTTCACTGGATTGAACTCACCGTTATCTTATTTTCATA 180
QY 26 -----LeuAsp 27
DB 181 CTTTATATGACTCAGCTGATCGATTAAGAAGCTTATTCGCCCTTGCTGTGAT 240
QY 28 IleLeuAsnSerIeuVaThrThrValPhenMetLeuIleLeuSerValLeuAlaLeuIle 47
DB 241 ATTACAACACTACTGGTACACAGTATTCATGCTCAACGTTGCTGTTGGCAGCTGATA 300

QY 48 ProGluThrThrIleThrValGlyGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 301 CCAGAACACACATGAGCTGAGTTGGGGGTGTTGCACITGTGACAGCAGTATGC 360
QY 68 CysLeuAlaAspGlyValLeuIleYArgLysLeuLeuPheIleProSerGlyProIyr 87
Db 361 TGTCTTGCGCGAGGGCCCTTATTAACCGGAGCTCTGTCATCCACCCAGGGCTCTAC 420
QY 88 GluLysProValHisGluLysGluValLeu 99
Db 421 CAGAAAAGGCTGTCATGAAAAAAAGAGTUTTG 456

Search completed: June 25, 2003, 12:51:07
Job time : 217 secs

GenCore Version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on : June 25, 2003, 12:33:06 ; Search time 65 Seconds

(without alignments)
467.092 Million cell updates/sec

Title:

US-09-801-115B-2

Perfect score: 508

Sequence: 1 MDNVQPKIKHRPFCCFSVKGH.....LFNPSPGPyQKKPVHEKKEVL 99

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
DelOp 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA
-LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=Blosum62 -TRANS=human40.cdi
-LIST=45 -DCALIGN=200 -THR_SCORE=PCT -THR_MIN=0 -THR_MATCH=0.1 -LOOPCL=0
-MODE=LOCAL -OUTFMT=PCT ; NORMEXT -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0980115 @CEN_1_L_61.ernrunat_20062003_141103_13607 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCITS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	508	100	504	4 US-09-149476-98
2	508	100	506	4 US-09-149476-252
3	357	70	392	4 US-09-385982-95
4	83	16	3	37948 4 US-09-251645-11
5	73	14	4	1083 4 US-09-116498-11
6	71	14	1083	4 US-09-116498-7
7	66	13	720	1 US-09-061092A-7
8	66	13	4403765	4 US-09-103840A-2
9	66	13	4411529	4 US-09-103840A-1
10	65	12	43676	3 US-09-165396-12
11	65	12	3872	4 US-09-165396-1
12	64.5	12	1333	1 US-08-684862-9

RESULT 1

US-09-19-476-98

; Sequence 98 Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: P2002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,623

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,622

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,621

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,620

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,619

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,618

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,616

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,614

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,613

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,612

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,611

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,610

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,609

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,608

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,607

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; EARLIER APPLICATION NUMBER: 60/047,606

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,605

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,604

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,603

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,602

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,601

; EARLIER FILING DATE: 1997-05-23

ALIGNMENTS

Sequence 1, Appl

Sequence 14, Appl

Sequence 167, App

Sequence 319, App

Sequence 2, Appl

Sequence 213, App

Sequence 12, Appl

Sequence 14, Appl

Sequence 9, Appl

Sequence 1, Appl

Sequence 37, Appl

Sequence 37, Appl

Sequence 62, Appl

EARLIER APPLICATION NUMBER: 60/056, 875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048, 964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057, 650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056, 884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057, 669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER FILING DATE: 1997-10-02

Alignment Scores:
 aligned: 2.43e-66 Length: 504
 core: 508/00 Matches: 99
 percent Similarity: 100.00% Conservative: 0
 test Local Similarity: 100.00% Mismatches: 0
 query Match: 100.00% Indels: 0
 B: 4 Gaps: 0

S-09-801-115B-2 (1-99) x US-09-149-476-98 (1-504)

1 MetaspasnvalGlnProlylSleYhsArgPropheCysPheSerValYsGlyHs 20
131 ATGGATAACGTGCAGGCCGAAATANACATGCCCTCTCTCTCAGTGTCAAAGCCAC 190
21 VallysMetMetIeuArgLeuAspIleLeaSerLeuValWthRthValPheMetIeuLe 40
191 GTGAAGATGCGCGCCGGATTATCAACTCACHTGTAACACAGATTCATGCCATC 250
41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyGlyValPhe 60
251 GTATCTGTGTGGACTGATACCGAACACAAATGACAGTGTTGGGAGGGGTT 310
61 AlaLeuValThrAlaValCysLeuIaAspGlyValAlaLeuLeuIleLeuGlyLeu 80
311 GCACTGTGCAAGCAGTAGTGTGTGCCACGGGGCCATTATCACCGAACGCTCTG 370
81 PheasnProSerGlyProtryglnlysLysProValHsGluLysGluValLeu 99
371 TTCATCCAGGGCTTACAGAAAAAAGCCTGNGCATGAAAAAAGAAGTTTC 427

RESULT 2

US-09-149-476-252
Sequence 252, Application US/09149476
Patent No. 6420536

GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149, 476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: 60/040, 162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038, 621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 334
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047, 600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 974

FILE REFERENCE: CCDDNA-260XX
 CURRENT APPLICATION NUMBER: US/09/385,982
 CURRENT FILING DATE: 1999-08-30
 EARLIER APPLICATION NUMBER: 09/328,111
 EARLIER FILING DATE: 1999-06-08
 EARLIER APPLICATION NUMBER: 60/117,393
 EARLIER FILING DATE: 1999-01-27
 EARLIER APPLICATION NUMBER: 60/098,639
 EARLIER FILING DATE: 1998-08-31
 NUMBER OF SEQ ID NOS: 544
 SOFTWARE: FastSEQ for Windows Version 3.0
 ;
 SEQ ID NO 95
 LENGTH: 392
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(392)
 OTHER INFORMATION: n = A,T,C or G
 ;
 US-09-385-982-95
 Alignment Scores:
 Pred. No.: 4.43e-44 Length: 392
 Score: 357.00 Matches: 71
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 16
 Query Match: 70.28% Indels: 20
 DB: 4 Gaps: 5
 ;
 US-09-801-115B-2 (1-99) x US-09-385-982-95 (1-392)
 QY 26 LeuAspIleLeuIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAla 45
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 44 CTTGATATTCACACTGCTAACACAGTGCATCTTATCCTGTTGGCA 103
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 46 LeuIleProGluThrThrThrLeuIleValGlyGlyValPheAlaLeuValThrAla 65
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 104 CTTGATACGAGAACGACATGACAGTTGGGGTGCTGAGAGCA 163
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 66 ValCysCysLeuIleAspGlyAlaLeuIleTyroGlyLeuIleAsnProSerylGly 85
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 164 GTATGCTGCTGCGGAGGCCATTATGCCGGAGCTGTGCAATCCACCGT 223
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 4
 QY 86 ProTyrglnLysProValHisGluLysLys 96
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 224 CCTTACCGAAAGCCCTGTGCAAAAAAA 256
 ;
 US-09-251-645-11
 Sequence 11, Application US/09251645
 ;
 Patent No. 6281413
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Vance C.
 ;
 APPLICANT: Morgan, Michael K.
 ;
 APPLICANT: Anderson, Arne R.
 ;
 APPLICANT: Hart, Hope
 ;
 APPLICANT: Warren, Gregory W.
 ;
 APPLICANT: Dunn, Martha
 ;
 APPLICANT: Chen, Jeng S.
 ;
 TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
 ;
 TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
 ;
 FILE REFERENCE: CGC1963/A
 ;
 CURRENT APPLICATION NUMBER: US/09/251,645
 ;
 CURRENT FILING DATE: 1999-02-17
 ;
 NUMBER OF SEQ ID NOS: 22
 ;
 SOFTWARE: PatentIn Ver. 2.0
 ;
 SEQ ID NO 11
 LENGTH: 37948
 TYPE: DNA
 ORGANISM: Photorhabdus luminescens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (15171)..(18035)
 ;
 OTHER INFORMATION: orf5
 ;
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (23768)..(31336)
 OTHER INFORMATION: hph2
 ;
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (31393)..(35938)
 OTHER INFORMATION: orf2
 ;
 US-09-251-645-11
 Alignment Scores:
 Pred. No.: 1.93 Length: 37948
 Score: 83.00 Matches: 28
 Percent Similarity: 51.76% Conservative: 16
 Best Local Similarity: 32.94% Mismatches: 21
 Query Match: 16.34% Indels: 20
 DB: 4 Gaps: 5
 ;
 US-09-801-115B-2 (1-99) x US-09-251-645-11 (1-37948)
 QY 12 ProPheCysPheSerValIysGlyHisValIysMetLeuArgLeuAspIleLeuSer 31
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 6476 CCATATGTCCTCTAGGAATGACCGAATCACAAACCTTAACAGT 6535
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 32 LeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 51
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 6536 TTGATA-----CTATAGTATTATGGGTCAAATAAATGCTATGAGAAAGCTACGAA 6589
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 52 ThrLeu-----ThrValGlyGlyGlyValPheAlaLeuValThrAla 65
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 6590 TCCCCTCATCGTAATAGTAAACGGTTATGATGGGAGATGGCTATC----TGA 6643
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 66 ValCysCysLeuIleAspGlyAlaLeuIleTyroGlyLeuIlePheAsnProSer 84
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 6644 GTATGCTGTTGGCGCA-----ATATTCAGCCATCACAC 6679
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 85 ---GlyProTyrgln 88
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 6680 TGGAGGTTCTCATCAG 6694
 ;
 RESULT 5
 Sequence 11, Application US/09116498
 ;
 Patent No. 6251582
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Littman, Dan R.
 ;
 Deng, Hongkui
 Unutuaz, Derya
 Ramani, Vineet N.K.
 ;
 TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
 ;
 ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
 IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
 THEREOF
 ;
 NUMBER OF SEQUENCES: 18
 ;
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 ;
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/116,498
 FILING DATE: 16-Jul-1998
 CLASSIFICATION: <Unknown>
 ;
 ATTORNEY/AGENT INFORMATION:
 ;

COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/061,092A
 FILING DATE: 14-MAY-1993
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Meuth, Donna M
 REFERENCE/DOCKET NUMBER: 018797-014
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (703) 836-6620
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 720 base pairs
 TYPE: nucleic acid
 STRANDBEDNESS: double
 TOPOLGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..720
 Alignment Scores:
 Pred. No.: 1.51
 Score: 66.50
 Percent Similarity: 48.61%
 Best Local Similarity: 30.56%
 Query Match: 13.09%
 DB: 1
 DB:
 US-09-801-115B-2 (1-99) x US-09-061-092A-2 (1-720)
 QY 28 IleIleAsnSerLeuValThrIlePheMetLeuIleLeuValSerLeuLeu----- 44
 Db 684 GTAGACCATAGCATAGTAAAGCACTATAGTAGTAAAGAGCAGATAGACGGCAGT 625
 QY 45 AlalLeuIleProGluLhrThrThrIleThrIleValGly-----GlyGlyIleAlaLeu 62
 Db 624 GTCCTCAGAGTCAGCTGCTGAAGGTAGGCCGCGTTGGAGGA----- 577
 QY 63 ValThrIlaValCysCysIleuaLaLaspGlyIleAlaLeuIleTyraTgLyS----- 78
 Db 576 -----TGTGCTGCTGTTATACTGGCTTGCCCTGGATTTCGGTCATATACAGTATT 523
 QY 79 -----LeuIlePheAsnProSerGlyProTyrgin 88
 Db 522 ACCATTCTCAGGATGATCCATCCACCATTCAG 487
 RESULT 8
 US-01-103-840A-2/C
 ; Sequence 2, Application US/09103840A
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1
 Alignment Scores:
 Pred. No.: 5.04e+05
 Score: 66.00
 Percent Similarity: 44.57%
 Best Local Similarity: 28.26%
 Query Match: 12.99%
 DB: 4
 DB:
 US-09-801-115B-2 (1-99) x US-09-103-840A-1 (1-4411529)
 QY 8 IleIlyHisArgProPhcysPheSerValIysGlyHistValIysMetLeuArgLeuAsp 27
 QY 8 IleIlyHisArgProPhcysPheSerValIysGlyHistValIysMetLeuArgLeuAsp 27
 Db 1499257 CTGGAGCCAGGAGCACACCAAGAATGGCTTGCCGGTGTGCGCGTGCCTATCG 1499198
 QY 28 IleIleAsnSerLeuValThrIlePheMetLeuIleLeuValSerLeuLeuAlaLeu 47
 Db 1499197 GGGCCGAGCIGTGGCCACCGAGGTTGCCCCGTCACGACCCATATGACC----- 1499144
 QY 48 ProGlutIleThrThrIleIleThrValGlyGlyIleAlaLeuIleValIysMetLeu 67
 Db 1499143 -----TGGCAACGCTGACATGGCGGATGGCGTGTGACGGCATGGGC 1499090
 QY 68 GlyIlyLysProValHisGluIlyLysGluValLeu 99
 Db 1499041 CAG -----CAGCAGATGCGGGATCTC 1499018
 RESULT 9
 US-09-03-840A-1/C
 ; Sequence 1, Application US/09103840A
 ; PATENT NO: 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1
 Alignment Scores:
 Pred. No.: 5.04e+05
 Score: 66.00
 Percent Similarity: 44.57%
 Best Local Similarity: 28.26%
 Query Match: 12.99%
 DB: 4
 DB:
 US-09-801-115B-2 (1-99) x US-09-103-840A-1 (1-4411529)
 QY 8 IleIlyHisArgProPhcysPheSerValIysGlyHisValIysMetLeuArgLeuAsp 27

|||||||
Db 1498059 CTGGAGCACAGGAGAACACCGAATCGGCCTCGGGGGCTCGGCGCCTCGGCATCG 1498000 ; Patent No. 6441134
Qy 28 IleIeleanSerIeauValThrThrValPheMetLeuIeValSerValLeuAlaLeuIle 47 ; GENERAL INFORMATION:
Db 1497999 GTCGCCGAGCTGTTGGCCAGGTTGTCGCCGCGCAAGACCCPAAATGACC----- 1497946 ; APPLICANT: BECKER, JEFFREY W.
Qy 48 ProgluthrThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCys 67 ; TITLE OF INVENTION: ISOLATED CANDIDA ALBICANS OLIGOPEPTIDE TRANSPORTER GENE
Db 1497945 -----TCGGCAACGCTGACATCGGGGGCTTGACGGATGGCCACCGCATGGGC 1497892 ; FILE REFERENCE: 372_6520P
Qy 68 CysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeuIleAsnProSerGlyProTrp 87 ; CURRENT APPLICATION NUMBER: US/09/1165, 396
Db 1497891 CTGACTGGAGACGCCCT-----TGGGCGGCCCTG-----GACGTGGCTCGGCCTTC 1497844 ; CURRENT FILING DATE: 1998-10-02
Qy 88 GlyLysLysProValHisGluLysLysGluValLeu 99 ; EARLIER APPLICATION NUMBER: PCT/US98/02332
Db 1497843 CAG-----CAGCAGAGTCGGGAACCTC 1497820 ; EARLIER FILING DATE: 1997-02-07
RESULT 10 ; NUMBER OF SEQ ID NOS: 15
; Sequence 12, Application US/09356952 ; SOFTWARE: PatentIn Ver. 2.0
; Patient No. 6117663 ; SEQ ID NO 1
; GENERAL INFORMATION: ; LENGTH: 3872
; APPLICANT: Borlack,Sjodin, Ann ; TYPE: DNA
; APPLICANT: Margarit, S. M. ; ORGANISM: C. albicans
; APPLICANT: Cole, Dafna ; FEATURE:
; APPLICANT: Cole, Phillip ; NAME/KEY: CDS
; APPLICANT: Kuriyan, John ; TITLE: DNA
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228N ; ALIGNMENT SCORES:
; CURRENT APPLICATION NUMBER: US/09/355, 952 ; Pred. No.: 30.7
; CURRENT FILING DATE: 1999-07-19 ; Score: 65.00
; EARLIER APPLICATION NUMBER: 60/093, 631 ; Matches: 16
; EARLIER FILING DATE: 1998-07-21 ; Percent Similarity: 55.32%
; NUMBER OF SEQ ID NOS: 14 ; Best Local Similarity: 34.04%
; SOFTWARE: PatentIn Ver. 2.0 ; Mismatches: 21
; SEQ ID NO 12 ; Indels: 0
; LENGTH: 43676 ; Gaps: 0
; TYPE: DNA ; DB:
; ORGANISM: Saccharomyces cerevisiae ; US-09-165-396-1 (481..2106, 2165..2887)
; US-09-356-952-12 ; US-09-165-396-1 (1-3872)
Alignment Scores:
Pred. No.: 30.7 Length: 3872
Score: 65.00 Matches: 16
Percent Similarity: 55.32% Conservative: 10
Best Local Similarity: 34.04% Mismatches: 21
Query Match: 12.80% Indels: 0
DB: 4 Gaps: 0
US-09-801-115B-2 (1-99) x US-09-165-396-1 (1-3872)
Qy 32 LeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluthrThr 51 ;
Db 1876 CTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 1935 ;
Qy 52 ThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCysCysLeuAlaASP 71 ;
Db 1936 GAATGCCAGTATGGGTTACGTTTGCTCTATATCGCTATCGCTATCGCTATTTTATACCC 1995 ;
Qy 72 GlyAlaLeuIleTyArgLys 78 ;
Db 1996 GTGGCTCATCATATTGCCAAA 2016 ;
RESULT 12 ;
US-08-084-862-9/C ;
; Sequence 9, Application US/08684862 ;
; Patent No. 579541 ;
; GENERAL INFORMATION: ;
; APPLICANT: Bach, Alfred ;
; APPLICANT: Bialojan, Siegfried ;
; APPLICANT: Hillen, Heinz ;
; TITLE OF INVENTION: No. 579541el Proteins, the Preparation and Use ;
; TITLE OF INVENTION: Theef ;
; NUMBER OF SEQUENCES: 14 ;
; CORRESPONDENCE ADDRESS: ;
; ADDRESSEE: Keil & Weintraub ;
; STREET: 1101 Connecticut Avenue ;
; CITY: Washington ;
; STATE: D.C. ;
; COUNTRY: USA ;
; ZIP: 20036 ;
; COMPUTER READABLE FORM: ;
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage ;
; COMPUTER: IBM AT-compatible, 80286 processor ;
; OPERATING SYSTEM: MS-DOS Version 5.0 ;
; SOFTWARE: WordPerfect version 5.1 ;
; CURRENT APPLICATION DATA: ;
; APPLICATION NUMBER: US/08/684, 862 ;
; FILING DATE: ;
; CLASSIFICATION: 435 ;
; PRIORITY APPLICATION DATA: ;
; sequence 1, Application US/09165396 ;
; sequence 1, Application US/09165396 ;

Pred. No.: 101 Length: 7721 ; STRANDENESS: double
 Score: 64.50 Matches: 23 ;
 Percent Similarity: 39.60% Conservative: 17 ;
 Best Local Similarity: 22.77% Mismatches: 30 ;
 Query Match: 12.70% Indels: 31 ;
 DB: 3 Gaps: 4

TOPLOGI: linear

US-09-801-115B-2 (1-99) x US-08-772-270A-14 (1-7721)

QY 22 LysMetLeuArgLeuAspLeuLeuSer-----LeuValThr 34
 Db 7519 CGTGTCTTCAGCATTGCTTAATGCTGAACTTAATGAACTGATACCA 7460
 QY 53 LeuThrValGlyGlyGlyValPheAlaLeuValThrAlaVal----- 66
 Db 7399 TTATCACCATCTGTTAATGTTCTGTGTAATCTCATAATAAGAATTAACCA 7340
 QY 67 -----CysCysLeuAlaAspGlyAlaLeuLeuThrValGlyGly 77
 Db 7339 AGCTGAGGGTGCTGATGCATGATGAGCTAATGAGTAACTGTTACCTTCCGATAGAGATACCA 7280
 QY 78 -----LysLeuLeuPheAsnProSerGlyProTyrglnLys 90
 Db 7279 TATCTGCTTAGGGAAAGTTCCACTTTAATRACTGCTTCCGATTCACAAA 7220

QY 91 PRO 91
 Db 7219 CCA 7217
 RESULT 15
 US-08-976-259-70
 ; Sequence 70, Application US/08976259

Patent No. 6316609 Search completed: June 25, 2003, 13:33:51
 GENERAL INFORMATION: Job time : 1226 secs

APPLICANT: Dillon, Patrick J. ;
 APPLICANT: Choi, Gil H. ;
 APPLICANT: Rodney A. ;
 TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
 Patient No. 6316609
 NUMBER OF SEQUENCES: 142
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stearn, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Ave, N.W., Suite 600
 CITY: Washington
 STATE: DC USA
 COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/976,259
 FILING DATE: Hereworth
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
 ATTORNEY/AGENT INFORMATION:
 NAME: Steffe, Eric K.
 REGISTRATION NUMBER: 36,688
 REFERENCE DOCKET NUMBER: 1488.0740002/EKS/CBM

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 70:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17710 base pairs
 TYPE: nucleic acid

STRANDENESS: double

TOPLOGI: linear

US-09-801-115B-2 (1-99) x US-08-976-259-70 (1-17710)

QY 4 ValGlnProLysIleLysHisArgProProheCysPheSerVal----- 17
 Db 17166 GTCAGGGTATGCTGCGATGATGATTTCGAGGCCAGCCGACTGTCG 17225
 QY 32 LeuValThrValPheMetLeuLeuValSerValAlaLeuLeuProGluThrThr 51
 Db 17286 CTGGTGACATCTGCGACGGTGACTCTGTCACAACCGGCCCTGAGATGATCAAATGTTG 17345
 QY 52 ThrLeuThrValGlyGlyGlyValPheAla-----LeuValThrAlaValCysCysLeu 69
 Db 17346 CGGGGACGGATCTGGTGGCGCAGTCATCAGGAATCTGCGCGCAGTCCTGCTG 17405
 QY 70 AlaAspGlyAlaLeu-----IleTygArgLysAsnProSerGlyProTyg 87
 Db 17406 GCAGGTGGTGGCTGTCGGGTCAGGGGGGGGATATTGTCAGTCCACTGGGACATT 17455

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2003, 13:13:19 ; Search time 135 Seconds

(without alignments)
1076.113 Million cell updates/sec

Title:

US-09-801-115b-2
Perfect score: 508

Sequence: 1 MDNVQPKIKHRPFCCSVKGH.....LFNPSPGYQKKPVHEKKEVL 99

Scoring table:

BLOSUM62

Xgapext 10.0 , Xgapbext 0.5
Ygappop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
DelOp 6.0 , Delext 7.0

Searched:

1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters:

2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+P2n.model1 -DEV=x1P
-0=/gn2_1/rspool/US0980115/runat_20062003_141105_13685/app_query.fasta_1.263
-DB=published_Applications_NA -QFMT=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-LONG=human40 cdi -LSIM=45 -DOCALIGN=200 -THR SCORE=0 -THR MAX=100
-THR MIN=0 ALIGN=15 MODE=LOCAL OUTFILE=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0980115 @CGN 1.1.80 @runat_20062003_141105_13685
-NCPU=6 -TCPBU=3 -NO_MMAP -LARGESEQS=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOp=10 -YGAPEXT=0.5 -DELOp=6 -DELExt=7

Database :

Published_Applications_NA:*

1: /cgn2_6/podata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/podata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/podata/1/pubpna/US05_NEWPUB.seq:*
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11: /cgn2_6/podata/1/pubpna/US10_NEWPUB.seq:*
12: /cgn2_6/podata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/podata/1/pubpna/US60_NEWPUB.seq:*
14: /cgn2_6/podata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	508	100.0	422	9 US-09-918-995-6534 Sequence 6534, App
2	508	100.0	439	9 US-09-8222-846-397 Sequence 397, App
3	508	100.0	504	9 US-09-809-391-98 Sequence 98, App
4	508	100.0	506	9 US-09-809-391-252 Sequence 252, App

ALIGNMENTS

RESULT 1
US-09-918-995-6534
; Sequence 6534, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09-918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: RSTSeq for Windows Version 3.0
; SEQ ID NO 6534
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-918-995-6534

Alignment Scores:
Pred. No.: 1.07e-63 Length: 422
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-801-115B-2 (1-99) x US-09-918-995-6534 (1-422)

QY 1 MetAspAsnValGlnProLysIleLysIleArgProHeCysPheSerVallysGlyHis 20
 Db 31 ATGGATAACCTGCAGCCAAATAAACATGCCCTCTGCCTCAGTGTGAAGGCCAC 90
 QY 21 VallysMetLeuArgLeuAspIleLeAsnSerLeuValThrThrValPheMetLeuIle 40
 Db 91 GTGAGATGCTGCCGCTGGATATTCAACTCACHTAACATGCTTCAGTGAAAGGCCAC 150
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuValThrValPheMetLeuIle 60
 Db 151 GTACTGTTGCGACTGATACCAGAACACATGACAGTGTGGAGGGCTT 210
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleThrArglyValphe 80
 Db 211 GCACTGTCAGACGAGTGTGCTTCGCCGACGGGCCCTTATTACGGGAGCTCTG 270
 QY 81 PheAsnProSerGlyProTyroGlnLysIlsProValHisGluLysGluValleu 99
 Db 271 TTCAATCCCAGGGCTTACAGAAAAGCCGTGCTGAAAGAAGTTCG 327

RESULT 2

US-09-822-846-397

; Sequence 397, Application US/09822846

; Publication No. US20030027139A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John M.

; APPLICANT: Lavalle, Edward R.

; APPLICANT: Collins-Racie, Lisa A.

; APPLICANT: Evans, Cheryl

; APPLICANT: Merberg, David

; APPLICANT: Treacy, Maurice

; APPLICANT: Agostino, Michael J.

; APPLICANT: Steininger II, Robert J.

; APPLICANT: Bowman, Michael R.

; APPLICANT: Spaulding, Vikki

; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary

; APPLICANT: Fechtel, Kim

; APPLICANT: Howes, Steven H.

; APPLICANT: Resnick, Richard J.

; APPLICANT: Gulukota, Kamalakar

; APPLICANT: Graham, James R.

; APPLICANT: Genetics Institute, Inc.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

FILE REFERENCE: GIN 6400

CURRENT APPLICATION NUMBER: US/09-822-846

CURRENT FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: 60/195, 605

PRIOR FILING DATE: 2000-04-06

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 397

LENGTH: 439

TYPE: DNA

ORGANISM: Homo sapiens

US-09-809-391-98

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Percent Similarity:	Best Local Similarity:	Mismatches:	Indels:	Gaps:
	508.00	504	99	100.0%	100.0%	0	0	0

DB:

US-09-801-115B-2 (1-99) x US-09-809-391-98 (1-504)

QY 1 MetAspAsnValGlnProLysIleLysIleArgProHeCysPheSerVallysGlyHis 20
 Db 131 ATGGATAACCTGCAGCCAAATAAACATGCCCTCTGCCTCAGTGAAAGGCCAC 190
 QY 21 VallysMetLeuArgLeuAspIleLeAsnSerLeuValThrThrValPheMetLeuIle 40
 Db 191 GTGAGATGCTGCCGCTGGATATTCAACTCACHTAACATGCTTCAGTGAAAGGCCAC 250
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuValThrValPheMetLeuIle 60
 Db 251 GTACTGTTGCGACTGATACCAGAACACATGACAGTGTGGAGGGCTT 310
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleThrArglyValphe 80
 Db 311 GCACTGTCAGACGAGTGTGCTTCGCCGACGGGCCCTTATTACGGGAGCTCTG 370
 QY 81 PheAsnProSerGlyProTyroGlnLysIlsProValHisGluLysGluValleu 99
 Db 371 TTCAATCCCAGGGCTTACAGAAAAGCCGTGCTGAAAGAAGTTCG 427

RESULT 4

US-09-809-391-252

; Sequence 252, Application US/09809391

; Publication No. US20030049618A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 252
LENGTH: 506
TYPE: DNA
ORGANISM: Homo sapiens
US-09-809-391-252

Alignment Scores:
Pred. No.: 1.4e-63 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-809-391-252 (1-506)

QY 1 MetAspAsnValGlnProLysIleLySHisArgProPheCysPheSerValLysGlyHis 20
Db 152 ATGGTAACTGCAGCCGAATAAACATGCCCTCTCTCGTGAAGGCCAC 211
Length: 506
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

QY 21 ValLysMetLeuArgLeuAspIleLeuAsnSerLeuValThrValPheMetLeuile 40
Db 212 GTGAGATGCGGCGCTGGATATTCACACTCACTGGTACACAGTTATGCATGCATC 271
Length: 506
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuIleValGlyGlyValPhe 60
Db 272 GTATCGTGTGTTGGCATGATACAGAACACACATGACAGTGGTGGAGGGTGTT 331
Length: 506
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

QY 61 AlaLeuValThrAlaValCysCysLeuIaAspCysAlaLeuIleTyrArgLeuIle 80
Db 332 GCACGTGACAGERTGATGCTGTTSCGACGGGCCATTACGGAGCTCTG 391
Length: 506
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

QY 81 PheAlaProSerGlyProTyrglyIlysProvalIhsGluLysGluValLeu 99
Db 392 TTCAATCCCAGGGCCTTACAGAAAAGCTGTGATGAAAGAAAAGAAGTTTG 448
Length: 506
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

RESULT 6

US-10-106-698-1927
Sequence 1927, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
FILE REFERENCE: PA0051
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-05-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564.0
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 1927
LENGTH: 558
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (514)..(514)
OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1927

Alignment Scores:
Pred. No.: 1.62e-63 Length: 558
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x US-10-106-698-1927 (1-558)

QY 1 MetAspAsnValGlnProLysIleLySHisArgProPheCysPheSerValLysGlyHis 20
Db 147 ATGGTAACTGCAGCCGAATAAACATGCCCTCTCTCGTGAAGGCCAC 206
Length: 558
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

QY 21 ValLysMetLeuArgLeuAspIleLeuAsnSerLeuValThrValPheMetLeuile 40
Length: 558
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

Alignment Scores:

QY 1 MetAspAsnValGlnProLysIleLySHisArgProPheCysPheSerValLysGlyHis 20
Db 152 ATGGTAACTGCAGCCGAATAAACATGCCCTCTCTCGTGAAGGCCAC 211
Length: 534
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

QY 21 ValLysMetLeuArgLeuAspIleLeuAsnSerLeuValThrValPheMetLeuile 40
Length: 534
Matches: 99
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

Db 207 GTGAGAGAAGCTGGCCTGATATTCACTCACTGGTACACAGATTCATGCATC 266 ; GENERAL INFORMATION:
 Qy 41 ValSerValLeuAlaLeuIleProGluThrThrIleSerLeuValYArgLysPhe 60 ; APPLICANT: Ma, D.
 Db 267 GATCTGTTGCTGGCACTGATACAGAAACACATGGACAGTGGGGGTGTT 326 ; APPLICANT: Han, W.
 Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80 ; APPLICANT: Zhang, Y.
 Db 327 GCACCTGAGCAGCATGATGCTGCTGCGACGGGCCATTACCGGAAGCTCTG 386 ; APPLICANT: Song, Q.
 Qy 81 PheAsnProSerGlyProTyroGlnLysProValIleGluLysLeuValLeu 99 ; APPLICANT: Di, C.
 Db 387 TTCATCCAGCGGCTCTTACCGAAAAGCCCTGGCATGAAAAAGAGTTG 443 ; APPLICANT: Huang, J.
 RESULT 7 ; APPLICANT: Tang, J.
 US-09-918-995-19489 ; APPLICANT: Chen, G.
 ; Sequence 19489, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS cDNA LIBRARIES
 ; FILE REFERENCE: 20411-56
 ; CURRENT APPLICATION NUMBER: US/09/918-995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 19489
 ; LENGTH: 512
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(512)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-19489
 Alignment Scores:
 Pred. No.: 1.04e-62 Length: 512 ;
 Score: 502.00 Matches: 98 ;
 Percent Similarity: 98.99% Conservative: 0 ;
 Best Local Similarity: 98.99% Mismatches: 1 ;
 Query Match: 98.82% Indels: 0 ;
 DB: 9 Gaps: 0 ;
 US-09-801-115B-2 (1-99) x US-09-801-115-3 (1-459)
 Qy 1 MetaspasValGlnProLysIleYSHisArgProPheCysPheSerValLysGlyHs 20 ;
 Db 1 ATGGATAACCTGCAGCCGAAATAAACATGCCCTCTCTCAGTGAAAGGCCAC 60 ;
 Qy 21 ValYsmMetLeuArg----- ;
 Db 61 GTGAGATGCTGCCTGCACACTRACTGACATCTATGACCCTTTATCATGCACAA 120 ;
 Qy 25 ----- ;
 Db 121 GCCCTGAAACCATATATGTTATCAGGGATTGAAGTCACCGTTACTTATTCATA 180 ;
 US-09-801-115B-2 (1-99) x US-09-801-115-3 (1-459)
 Qy 26 ----- ;
 Db 181 CTTTATGTAATGACTGAGTGTGATGCTTAATGAGTGTATTGGCCCTTGCTGTATG 240 ;
 Qy 28 IleIleAsnSerLeuValThrThrIleValPhmetLeuIleLeuSerValLeuAlaLeu 47 ;
 Qy 21 ValYsmMetLeuArgLeuAspIleAspIleAspSerLeuValThrValPhmetLeuIle 40 ;
 Db 202 GTGAAGAGCTCGGGCTGATATTACACTGCTACAGTATCAGTCTACGTTGCTCATC 261 ;
 Qy 41 ValSerValLeuAlaLeuIleProGluThrThrIleLeuValYArgLysLeu 80 ;
 Db 262 GATCTGTTGCTGGCACTGATACAGAAACACATGGACAGTGGGGGTGTT 321 ;
 Qy 61 AlaLeuValThrAlaValCysCysteauAspGlyAlaLeuIleTyrArgLysLeu 80 ;
 Db 322 GCACCTGAGCAGCATGATGCTGCTGCGACGGGCCATTACCGGAAGCTCTG 381 ;
 Qy 81 PheAsnProSerGlyProTyroGlnLysProValIleGluLysLeuValLeu 99 ;
 Db 382 TTCATCCAGCGGCTCTTACCGAAAAGCCCTGGCATGAAAAAGAGTTG 438 ;
 RESULT 8 ; Sequence 189, Application US/09978295A
 US-09-978-295A-189 ; Patent No. US2002015605A1
 ; Sequence 3, Application US/09801115 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.	PRIOR APPLICATION NUMBER: 60/079798
APPLICANT: Botstein, David	PRIOR FILING DATE: 1998-03-27
APPLICANT: Desnoyers, Luc	PRIOR APPLICATION NUMBER: 60/079920
APPLICANT: Eaton, Dan	PRIOR FILING DATE: 1998-03-30
APPLICANT: Ferrara, Napoleone	PRIOR APPLICATION NUMBER: 60/079923
APPLICANT: Filvaroff, Ellen	PRIOR FILING DATE: 1998-03-30
APPLICANT: Fong, Sherman	PRIOR APPLICATION NUMBER: 60/080105
APPLICANT: Gao, Wei-Oolang	PRIOR FILING DATE: 1998-03-31
APPLICANT: Gerber, Hanspeter	PRIOR APPLICATION NUMBER: 60/080107
APPLICANT: Gerritsen, Mary E.	PRIOR FILING DATE: 1998-03-31
APPLICANT: Goddard, Audrey	PRIOR APPLICATION NUMBER: 60/080165
APPLICANT: Godowski, Paul J.	PRIOR FILING DATE: 1998-03-31
APPLICANT: Grimaldi, J. Christopher	PRIOR APPLICATION NUMBER: 60/080194
APPLICANT: Gurney, Austin L.	PRIOR APPLICATION NUMBER: 60/080328
APPLICANT: Hillian, Kenneth J.	PRIOR FILING DATE: 1998-04-01
APPLICANT: Klijavins, Ivar J.	PRIOR APPLICATION NUMBER: 60/080328
APPLICANT: Kuo, Sophia S.	PRIOR FILING DATE: 1998-04-01
APPLICANT: Napier, Mary A.	PRIOR APPLICATION NUMBER: 60/080333
APPLICANT: Pan, James;	PRIOR FILING DATE: 1998-04-01
APPLICANT: Paoni, Nicholas F.	PRIOR APPLICATION NUMBER: 60/080334
APPLICANT: Roy, Margaret Ann	PRIOR FILING DATE: 1998-04-01
APPLICANT: Sheldon, David L.	PRIOR APPLICATION NUMBER: 60/081070
APPLICANT: Stewart, Timothy A.	PRIOR FILING DATE: 1998-04-08
APPLICANT: Tumas, Daniel	PRIOR APPLICATION NUMBER: 60/091049
APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-04-08
APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/081071
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	PRIOR FILING DATE: 1998-04-08
FILE REFERENCE: P2630PIC11	PRIOR APPLICATION NUMBER: 60/081195
CURRENT APPLICATION NUMBER: US/09/978, 295A	PRIOR FILING DATE: 1998-04-08
CURRENT FILING DATE: 2001-10-15	PRIOR APPLICATION NUMBER: 60/081203
PRIOR APPLICATION NUMBER: 09/918585	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 2001-07-30	PRIOR APPLICATION NUMBER: 60/081229
PRIOR APPLICATION NUMBER: 60/062250	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1997-10-17	PRIOR APPLICATION NUMBER: 60/081259
PRIOR APPLICATION NUMBER: 60/064249	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1997-11-03	PRIOR APPLICATION NUMBER: 60/081264
PRIOR APPLICATION NUMBER: 60/065311	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1997-11-13	PRIOR APPLICATION NUMBER: 60/081270
PRIOR APPLICATION NUMBER: 60/066364	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1997-11-21	PRIOR APPLICATION NUMBER: 60/081270
PRIOR APPLICATION NUMBER: 60/067450	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1997-11-30	PRIOR APPLICATION NUMBER: 60/081270
PRIOR APPLICATION NUMBER: 60/077632	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-03-11	PRIOR APPLICATION NUMBER: 60/081270
PRIOR APPLICATION NUMBER: 60/077641	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-03-11	PRIOR APPLICATION NUMBER: 60/081270
PRIOR APPLICATION NUMBER: 60/077649	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-03-11	PRIOR APPLICATION NUMBER: 60/081270
PRIOR APPLICATION NUMBER: 60/077791	PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-03-12	PRIOR APPLICATION NUMBER: 60/082568
PRIOR APPLICATION NUMBER: 60/078004	PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-03-13	PRIOR APPLICATION NUMBER: 60/082569
PRIOR APPLICATION NUMBER: 60/078886	PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/082704
PRIOR APPLICATION NUMBER: 60/078936	PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/082804
PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/082700
PRIOR APPLICATION NUMBER: 60/078939	PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/082797
PRIOR APPLICATION NUMBER: 60/079294	PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-03-25	PRIOR APPLICATION NUMBER: 60/082796
PRIOR APPLICATION NUMBER: 60/079656	PRIOR FILING DATE: 1998-04-23
PRIOR FILING DATE: 1998-03-26	PRIOR APPLICATION NUMBER: 60/083336
PRIOR APPLICATION NUMBER: 60/079664	PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/079689	PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/083392
PRIOR APPLICATION NUMBER: 60/079663	PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/083495
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PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-03-27	PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-03-27	PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/083554

PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084666
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084411
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084337
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
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PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
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PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 3.66e-58 Length: 663 Qy 26 -----
Score: 471.50 Matches: 99 Db 311 CTTTATATGACTAGACTGTGATTATGAGTGGTTATTTGGCTTGTGAT 370
Percent Similarity: 65.13% Conservative: 0 28 IleIleAsnSerLeuValThrValPheMetIleUleValSerValLeuAlaLeuIle 47
Best local Similarity: 92.81% Mismatches: 0 371 ATTACAACTCACTGTACAGTATCATGCTCATGTAATCTGTTGGCACTGATA 430
Query Match: 9 Indels: 53 48 PROGLYRThrThrLeuLysValGlyGlyValPheAlaLeuValThrLalaValcys 67
DB: 191 GTGAAGATGCTGGCCTGCACTACTGTGACATCTACACCTTTATCATGCACAA 250 491 TGCTGCCACGGGCCCTATTACCGAAGCTCTCTGTCATCCAGCGGTCTAC 550
Qy 25 ----- 88 GlutLysLysProvalHisGluLysLysGluLeuIle 99
Db 551 CAGAAAAGCCTGNCATGAAAGAAAGAGTTTG 586

RESULT 10
US-09-978-697-189
; Sequence 189, Application US/09978697
; General Information:
; Patent No. US20020169284A1
; Applicant: Ashkenazi, Avi
; Applicant: Baker, Kevin P.
; Applicant: Botstein, David
; Applicant: Destroyer, Luc
; Applicant: Eaton, Dan
; Applicant: Ferrara, Napoleon
; Applicant: Flivarooff, Ellen
; Applicant: Fong, Sherman
; Applicant: Gao, Wei-Qiang
; Applicant: Gerber, Hanspeter
; Applicant: Gerittsen, Mary E.
; Applicant: Goddard, Audrey
; Applicant: Godowski, Paul J.
; Applicant: Grimaldi, J. Christopher
; Applicant: Gurney, Austin L.
; Applicant: Hillman, Kenneth J.
; Applicant: Kijaviv, Ivar J.
; Applicant: Kuo, Sophia S.
; Applicant: Napier, Mary A.
; Applicant: Pan, James
; Applicant: Paoni, Nicholas F.
; Applicant: Roy, Margaret Ann
; Applicant: Shelton, David L.
; Applicant: Stewart, Timothy A.
; Applicant: Tumas, Daniel
; Applicant: Williams, P. Mickey
; Applicant: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2530UPIC27
CURRENT APPLICATION NUMBER: US/09/978, 697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11

Qy 25 ----- Leuasp 27
Db 311 CTTTATATGACTAGACTGTGATTATGAGTGGTTATTTGGCTTGTGAT 370
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371 ATTACAACTCACTGTACAGTATCATGCTCATGTAATCTGTTGGCACTGATA 430
48 PROGLYRThrThrLeuLysValGlyGlyValPheAlaLeuValThrLalaValcys 67
491 TGCTGCCACGGGCCCTATTACCGAAGCTCTCTGTCATCCAGCGGTCTAC 550
88 GlutLysLysProvalHisGluLysLysGluLeuIle 99
551 CAGAAAAGCCTGNCATGAAAGAAAGAGTTTG 586

PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	3.66e-58	Length:	663
Score:	471.50	Matches:	99
Best Local Similarity:	65.13%	Conservative:	0
Query Match:	92.81%	Mismatches:	0
DB:	9	Indels:	53
		Gaps:	1

US-09-801-115B-2 (1-99) x US-09-978-697-189 (1-663)

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Qy 21 ValLysMetLeuArg----- 25

D0 191 GTGAGAGCTGGCTGGCTGGCACTAACTGTGACATCTATGACCTTTATCATCGCAC 250

Qy 25 ----- 25

Db 251 GGCCTGACCATATATGTTATCACTGAGTTGAACTACCGTTATCTTATTCATA 310

Qy 26 ----- 26

Db 311 CTTTTATGFACTCAGACTGATGCGATTATGAAGTGGTATTGGCTTGCTGAT 370

Qy 28 IleLeuAsnSerLeuValThrValThrAlaPheMetIleLeuValSerValLeuAlaLeuIle 47

Db 371 ATTATCACTCACTGACTACACAGATCTATGCTCATGCTATGCTATGCTG 430

Qy 48 ProGluThrThrLeuThrValGlyGlyGlyValPheLeuAlaLeuValThrAlaValCys 67

Db 431 CGAAACACACACAGTACAGTGGTGGAGGGGTTTGACCTGTCATCCGGCTTCAC 490

Qy 68 CysLeuAlaAspGlyAlaLeuIleIleArgLysLeuLeuIleAsnProArgGlyProIle 87

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Qy 88 GluLysLysProValHisGluLysGluValLeu 99

Db 551 CAGAAGAAAGCTGTGTCATGAAAAAAGAGTting 586

RESULT 11

US-09-978-192A-189

; Sequence 189, Application US/09978192A

; GENERAL INFORMATION:

; Patent No. US2002017553A1

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyes, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kujavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Poole, Nicholas F.

; APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tunas, Daniel
 APPLICANT: Williams, P. Mickey

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2630P1C9

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689

Alignment Scores:
Pred. No.: 3.668-58 Length: 663
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.818 Indels: 53
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x US-09-978-192A-189 (1-663)

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QY	21 VallysMetLeuArg-----	25
Db	191 GTGAAGATGCCGCGCTGGCACTAACTGTGACATCTATGACCTTTTATCATCGCACAA	250
QY	25 -----	25
Db	251 GCCCTGAACTATATTGTATCACTGGATTGAGTCACCGTTATCTTATTTCATA	310
QY	26 -----	26
Db	311 CTTTATATGACTAGACTGATGATTGAGTGTATTGCTTTCCTTGCTGT	370
QY	28 IleLeuAsnSerLeuValThr-ThrAlaPhenylLeuIleSerValLeuAlaLeuIle	47
Db	371 ATTATCACTCACTGGTAAACAGACTCATGCTATCGTATCGTGTGACTGATA	430
QY	48 ProGluIleThrIleLeuIleGlyAlaLeuLeuPheAsnProSerGlyProYr	87
Db	431 CCAGAAACACAACTGACAGTGTGGTGGAGGTTGACTGTGACAGCATGC	490
QY	68 CysLeuAlaAspGlyAlaLeuIleTyroGlyLeuLeuPheAsnProSerGlyProYr	87
Db	491 TGTCTTCCGAGGGGCCCTATTACCGGAGCTCTGTCACTCCAGCGGCTTAC	550
QY	88 GluIlysProValHisGluIlysGluValLeu	99
Db	551 CAGAAAAGCTGGCATGAAAAAARGAGTTG	586

US-09-999-832A-189
 Publication 189, Application US/09999832A
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William T.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Aids Encoding the Same
 FILE REFERENCE: P2430PIC63
 CURRENT APPLICATION NUMBER: US/09/999,832A
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1991-10-17
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 PRIOR FILING DATE: 1997-11-03
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 PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083499 QY 25 -----
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545 Db 251 GCCCCTGAAACCATATATTGTTACTGGATTAGTCAGCTTATTTCTATA 310
 PRIOR FILING DATE: 1998-04-29 QY 26 -----
 PRIOR APPLICATION NUMBER: 60/083558 |||||| Leuasp 27
 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083559 311 CTTTATATGTACTGAGCTGTGATTATGGAGTGGTTATTGGCTTGCCTGAT 370
 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083559 28 IleLeuAsnSerLeuValThrValPheMetIeuLeuValSerValLeuAlaLeuile 47
 PRIOR APPLICATION NUMBER: 60/083500 PRIOR APPLICATION NUMBER: 60/083500 371 ATTACAACTCAGTGAACACATGTCATCGTATCTGTTGGACTGATA 430
 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083742 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/084366 Db 431 CCAGAAACCACACTGACAGTGGAGGGGTGACTGTGACAGCAGTGC 490
 PRIOR FILING DATE: 1998-05-05 PRIOR APPLICATION NUMBER: 60/084414 QY 68 CysLeuAlaAspGlyValLeuIleLeuIleArgLysLeuLeuIeasnProSerGlyProTyR 87
 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/084637 491 TGCTCTGCCGAGGGGCCATTATCGGGAGCTCTGTCAACTCCAGGGCTCTAC 550
 PRIOR APPLICATION NUMBER: 60/084639 PRIOR APPLICATION NUMBER: 60/084640 QY 88 GluDysLysProValHisGluLysGlyValLeu 99
 PRIOR FILING DATE: 1998-05-07 551 CAGAAAAGCGCTGTCATGAAKAAAAGAAGTGTG 586
 PRIOR APPLICATION NUMBER: 60/084640 Db RESULT 13
 PRIOR FILING DATE: 1998-05-07 US-09-978-189-189
 PRIOR APPLICATION NUMBER: 60/084598 ; Sequence 189, Application US/09978189
 PRIOR FILING DATE: 1998-05-07 ; Publication No. US20030004102A1
 PRIOR APPLICATION NUMBER: 60/084600 ; GENERAL INFORMATION:
 PRIOR FILING DATE: 1998-05-07 ; APPLICANT: Ashkenazi, Avi
 PRIOR APPLICATION NUMBER: 60/084627 ; APPLICANT: Baker, Kevin P.
 PRIOR FILING DATE: 1998-05-07 ; APPLICANT: Bottstein, David
 PRIOR APPLICATION NUMBER: 60/084643 ; APPLICANT: Desnoyers, Luc
 PRIOR FILING DATE: 1998-05-07 ; APPLICANT: Eaton, Dan
 PRIOR APPLICATION NUMBER: 60/085339 ; APPLICANT: Ferrara, Napoleon
 PRIOR FILING DATE: 1998-05-13 ; APPLICANT: Filvaroff, Ellen
 PRIOR APPLICATION NUMBER: 60/085323 ; APPLICANT: Fong, Sherman
 PRIOR FILING DATE: 1998-05-13 ; APPLICANT: Gao, Wei-Qiang
 PRIOR APPLICATION NUMBER: 60/085582 ; APPLICANT: Gerber, HansPeter
 PRIOR FILING DATE: 1998-05-13 ; APPLICANT: Gerritsen, Mary E.
 PRIOR APPLICATION NUMBER: 60/085579 ; APPLICANT: Goddard, Audrey
 PRIOR FILING DATE: 1998-05-15 ; APPLICANT: Godowski, Paul J.
 PRIOR FILING DATE: 1998-05-15 ; APPLICANT: Grimaldi, J. Christopher
 PRIOR APPLICATION NUMBER: 60/085689 ; APPLICANT: Gurney, Austin L.
 PRIOR FILING DATE: 1998-05-15 ; APPLICANT: Hillian, Kenneth J.
 PRIOR APPLICATION NUMBER: 60/085579 ; APPLICANT: Klijavin, Ivar J.
 PRIOR FILING DATE: 1998-05-15 ; APPLICANT: Kuo, Sophia S.
 PRIOR APPLICATION NUMBER: 60/085580 ; APPLICANT: Napier, Mary A.
 PRIOR FILING DATE: 1998-05-15 ; APPLICANT: Pan, James
 PRIOR APPLICATION NUMBER: 60/085573 ; APPLICANT: Paoni, Nicholas F.
 PRIOR FILING DATE: 1998-05-15 ; APPLICANT: Roy, Margaret Ann
 PRIOR APPLICATION NUMBER: 60/085704 ; APPLICANT: Shelton, David L.
 PRIOR FILING DATE: 1998-05-15 ; APPLICANT: Stewart, Timothy A.
 ; PRIOR APPLICATION NUMBER: 60/085697 ; APPLICANT: Tumas, Daniel
 ; Alignment scores: ; APPLICANT: Williams, P. Mickey
 ; Pred. No.: 3.66e-58 ; APPLICANT: Wood, William I.
 ; Score: 471.50 ; Length: 663
 ; Percent Similarity: 65.13% ; Matches: 99
 ; Best Local Similarity: 65.13% ; Conservative: 0
 ; Query Match: 92.81% ; Mismatches: 0
 ; DB: 9 ; Inels: 53
 ; Gaps: 1
 US-09-801-115B-2 (1-99) x US-09-999-832A-189 (1-663)
 QY 1 MetAspPheNalGlnIleProIleLysIleSarProPropheCysPheSerValIleGlyIle 20
 Db 131 ATGGATAACCTGCAAGCCGAAATAAACATCGCCCTCTGCCTCAGTGTAAGGCCAC 190
 QY 21 ValIysMetLeuArg----- 25
 Db 191 GTGAGATGCTGCGGCTGCACTACTGACATCATGACCTTTATCATGCACAA 250

PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 ;
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
 Pred. No.: 3.66e-58 Length: 663
 Score: 471.50 Matches: 99
 Percent Similarity: 65.13% Conservative: 0
 best Local Similarity: 65.13% Mismatches: 0
 Query Match: 92.81% Indels: 53
 DB: Gaps: 1

US-09-801-115B-2 (1-99) x US-09-978-189-189 (1-663)

QY 1 MetAspAsnValGlnProLysIleTyrLysHisArgProHeCysPheSerValLysGlyHis 20
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 131 ATGGATAACGTGCAGCCAAATAAACATGCCCTCTCGTCAGTGCAAAGGCCAC 190

QY 21 VallysMetLeuArg----- 25

DB 191 GTGAGAATGCTGGCTGCACTAACCTGACATCTAGACCTTTATCATGCCACAA 250

QY 25 ----- 25

DB 251 GCCCTGACCATATATTGTTACTGAGTTGAACTCACGGTTAACGTTACCTTATTCATA 310

QY 26 ----- 26

DB 311 CTTTTATATGTAATCGACTGATCGATTAATGAAGTGTTATTGGCTTGCTGTAT 370

QY 28 IleIleAsnSerLeuValThrThrValPhenMetLeuLeuValSerValLeuAlaLeuIle 47

DB 371 ATTATCAACTCTACTGGPACACAGTTCTACGCTCATCGTATCTGGTACGATGATA 430

QY 48 ProGluThrThrThrLeuThrValGlyGlyIvalPhenAlaLeuValThrAlaValCys 67

DB 431 CCAGAACACACACATGACAGTTGGGGGTTGACTTGACGACAGCAGTAGTC 490

QY 68 CysLeuAlaAspGlyAlaLeuLeuTyrArgLysLeuLeuPheAsnProSerGlyProYR 87
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 491 TGTCTGGCGACGGGCCCTTAATACCGGAAGCTCTGTCATCCAGGGTCTTAC 550

QY 88 GluLysLysProValHisGluLysLysGluValLeu 99
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DB 551 CAGAAAAGCCCTGCGAAGAAAAAGAACTTTC 586

RESULT 14

; Sequence 189, Application US-09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritten, Mary E.
 APPLICANT: Goddard, Andrej
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavin, Ivar J.

APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Sheldon, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William I.
 APPLICANT: Williams, P. Mickey

APPLICANT: Williams, P. Mickey

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2630P1C2

CURRENT APPLICATION NUMBER: US-09-978-608A

CURRENT FILING DATE: 2001-10-16

NUMBER OF SEQ ID NOS: 624

Prior Application removed - See File Wrapper or Palm.

SEQ ID NO: 189

LENGTH: 663

TYPE: DNA

ORGANISM: Homo sapiens

US-09-978-608A-189

Alignment Scores:
 Pred. No.: 3.66e-58 Length: 663
 Score: 471.50 Matches: 99
 Percent Similarity: 65.13% Conservative: 0
 Best Local Similarity: 65.13% Mismatches: 0
 Query Match: 92.81% Indels: 53
 DB: Gaps: 1

US-09-801-115B-2 (1-99) x US-09-978-608A-189 (1-663)

QY 1 MetAspAsnValGlnProLysIleTyrLysHisArgProHeCysPheSerValLysGlyHis 20
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 131 ATGGATAACGTGCAGCCAAATAAACATGCCCTCTCGTCAGTGCAAAGGCCAC 190

QY 21 VallysMetLeuArg----- 25

DB 191 GTGAGAATGCTGGCTGCACTAACCTGACATCTAGACCTTTATCATGCCACAA 250

QY 25 ----- 25

DB 251 GCCCTGACCATATATTGTTACTGAGTTGAACTCACGGTTAACGTTACCTTATTCATA 310

QY 26 ----- 26

DB 311 CTTTTATATGTAATCGACTGATCGATTAATGAAGTGTTATTGGCTTGCTGTAT 370

QY 28 IleIleAsnSerLeuValThrThrValPhenMetLeuLeuValSerValLeuAlaLeuIle 47

DB 371 ATTATCAACTCTACTGGPACACAGTTCTACGCTCATCGTATCTGGTACGATGATA 430

QY 48 ProGluThrThrThrLeuThrValGlyGlyIvalPhenAlaLeuValThrAlaValCys 67

DB 431 CCAGAACACACACATGACAGTTGGGGGTTGACTTGACGACAGCAGTAGTC 490

QY 68 CysLeuAlaAspGlyAlaLeuLeuTyrArgLysLeuLeuPheAsnProSerGlyProYR 87
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 491 TGTCTGGCGACGGGCCCTTAATACCGGAAGCTCTGTCATCCAGGGTCTTAC 550

QY 88 GluLysLysProValHisGluLysLysGluValLeu 99
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DB 551 CAGAAAAGCCCTGCGAAGAAAAAGAACTTTC 586

RESULT 15

; Sequence 189, Application US-09978191A
; Publication No. US20030050339A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Olang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William L.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2630P1C4
 CURRENT APPLICATION NUMBER: US/09/978/191A
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
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PRIORITY FILING DATE: 1998-04-29
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PRIORITY APPLICATION NUMBER: 60/085580
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085573
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085704
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085697

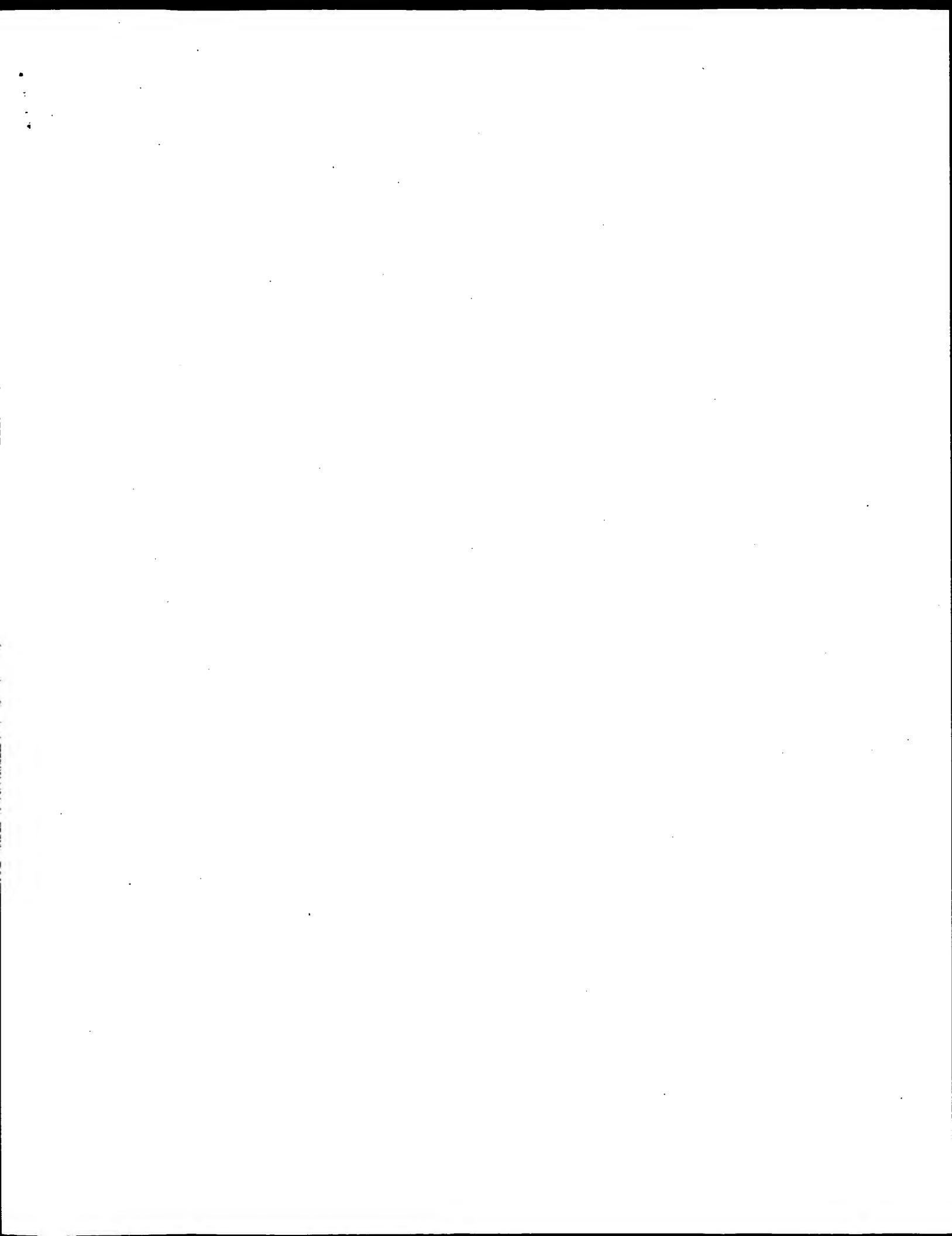
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Pred. No.: 3.66e-58 Length: 663
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.83% Indels: 53
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x US-09-978-191A-189 (1-663)

QY 1 MetAspAsnValGlnProTyrIleLysArgProPheCysPheSerValLeuGlyHis 20
Db 131 ATGGAAACGGCGAGCGAAATAAACATGCCCTTCGCTTCAGTGAAAGGCCAC 190
QY 21 ValLeuMetLeuArg----- 25
Db 191 GTGAGAGATGCTGGCTGGCACTAACTGIGACATCTATGACCTTTATCATGCACAA 250
QY 25 ----- 25
Db 251 GCCCTGAAACCATATGTATCACGGATTGAACTCACCGTTATCTTATTTCAATA 310
QY 26 ----- Leuasp 27
Db 311 CTTTAATAGTACTGAGACTGATGATTAATGAGGGTTATTTGCCCTTGCTGAT 370
QY 28 IleLeuAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
Db 371 ATTATCACTTCACTGGTAAACAGTATCATCTCACTGACTGCTTGCCACTGATA 430
QY 48 ProGlutThrThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 431 CCGAGAACACACACATGACAGTGGGGGTGTTGACTTGACAGCAGTG 490
QY 68 CysteLeuAlaAspGlyAlaLeuIleTyroGlyLeuLeuPheAsnProSerGlyProTyr 87
Db 491 TGTCTTGCGACGGGGCCCTATTTACCGAACATTCTGTCATCCAGCGTCCTAC 550
QY 88 GluIlysProValHisGluIlysGluValLeu 99
Db 551 CAGAAAAGCCTGTCATGAAAAAAAGAGTGTG 586

Search completed: June 25, 2003, 14:29:35
Job time : 138 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 06:26:50 ; Search time 1523 Seconds

(without alignments) 10204.135 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534

Sequence: 1 gttcccaatctgaaatgtaa...aaaaaaa...aaaaaaa 534

Scoring table: IDENTITY.NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: gb_hmg: *
3: gb_ln: *
4: gb_on: *
5: gb_ov: *
6: qb_ptp: *
7: qb_ph: *
8: qb_pl: *
9: qb_pr: *
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13: qb_un: *
14: qb_v1: *
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27: em_sis: *
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SUMMARIES

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4	349	65.4	593	9	AF145216	AF145216 Homo sapi
5	338	63.3	688	9	BC004380	BC004380 Homo sapi
6	325.4	60.9	655	9	AF057306	AF057306 Homo sapi
7	321.8	60.3	669	6	AX061665	AX061665 Sequence
8	316.4	59.3	434	9	AF135381	AF135381 Homo sapi
9	278	52.1	485	11	G30204	G30204 human SRS S
10	214.4	40.1	97083	9	AC010289	AC010289 Homo sapi
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13	205	38.4	207	6	AX330610	AX330610 Sequence
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16	205	38.4	207	6	AX08097	AX08097 Sequence
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18	184.8	34.6	180702	9	AC018557	AC018557 Homo sapi
19	165.4	31.0	523	10	AF253064	AF253064 Rattus no
20	158.4	29.7	6283	6	AX52053	AX52053 Sequence
21	158.4	29.7	6283	6	AX34431	AX34431 Sequence
22	158.4	29.7	6283	6	AX48836	AX48836 Sequence
23	135	25.3	568	10	AY047360	AY047360 Mus muscu
24	126	682	10	AF253065	AF253065 Rattus no	
25	119.4	22.4	6283	6	AX222052	AX222052 Sequence
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31	63.8	11.9	527	10	AY046597	AY046597 Mus muscu
32	55	10.3	268147	2	AC116966	AC116966 Dicytostele
33	54.2	10.1	100726	2	AC116961	AC116961 Dicytostele
34	53.8	10.1	30726	2	AC117269	AC117269 Dicytostele
35	53.4	10.0	55470	2	AC116989	AC116989 Dicytostele
36	53.4	10.0	182405	2	AC119586	AC119586 Rattus no
37	52.4	9.8	1926	10	BC008268	BC008268 Mus muscu
38	52.4	9.8	211759	2	AC106937	AC106937 Rattus no
39	51.8	9.7	17718	2	AC108297	AC108297 Rattus no
40	51.6	9.7	190735	2	AC109750	AC109750 Rattus no
41	51.4	9.6	2669	10	BC018270	BC018270 Mus muscu
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43	51	9.6	167878	2	AC099255	AC099255 Rattus no
44	50.6	9.5	224	3	DDIAC12	M23112 D. discoideum
45	50.6	9.5	2165	9	BC009565	BC009565 Homo sapi

ALIGNMENTS

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DLYRKLFWPLPVQPKPVHEKEVL"									
BASE COUNT	166	a	120	c	140	g	167	t	ORIGIN
Query Match	65.4%		Score	349;	DB	9;	Length	593;	
Best Local Similarity	79.8%		Pred.	No.	3.4e-75;				
Matches	465;	Conservative	0;	Mismatches	55;	Indels	63;	Gaps	2;
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	11	GGGAGCCGAGCTGGCGAGAAGTAGGGAGGGGGTGTCCGCCGCGGGGTGCT	70						
Qy	75	ATCGCTTCGAGAACCTACTCAGCGAGCAGCTGAGAAGAGTGAGGAAGTGTCTG	134						
	71	ATGCCCTCGCAGAACCTACTCAGCGAGCAGCTGAGAAGAGTGAGGAAGTGTCTG	130						
Qy	135	CTGGGTCTCGAGCGGAGTACACTCAGCGAGCAGCTGAGAAGAGTGAGGAAGTGTCTG	194						
	131	CTGGGTCTCGAGCGGAGTACACTCAGCGAGCAGCTGAGAAGAGTGAGGAAGTGTCTG	190						
Qy	195	TCACTGTGAAGGCCACGCGAGATGCTGGCGGTG-----	230						
	191	TCAGTGTGAAGGCCACGCGAGATGCTGGCGGTG-----	250						
Qy	231	-----ATATATCACTCTGGTACACACAG	257						
	251	TTTTATCATGGCACACCCCTGAAACATATGTTACCTGTTGAGTCACCG	310						
Qy	258	TATCTCATGCTCATGCTACTGTGTGACTGATACAGA-----AACACAAACATGA	311						
	311	TATCTCATTTTCACTCTTATGTTACTGAGCTGATGATTATGAGTGTAT	370						
Qy	312	CAGTGTGGAGGGTGTGTCAATCCAGGGTCTTACAGAAAMAGCCTGTGATG	371						
	371	TTRGGCCTTGCTGTGTTGACTTGACAGCAGTATGCTGCTGCGACGGGCC	430						
Qy	372	TTATTCGGGAAGCTGTGTCAATCCAGGGTCTTACAGAAAMAGCCTGTGATG	431						
	431	TTATTCGGGAAGCTGTGTCAATCCAGGGTCTTACAGAAAMAGCCTGTGATG	490						
Qy	432	AAAAAAAAGAAGTTGTAATTATTAATCTTGTGTGATCTAAGTTAAACAT	491						
	491	AAAAAAAAGAAGTTGTAATTATTAATCTTGTGTGATCTAAGTTAAACAT	550						
Qy	492	ATTTCTTATTCCTCCAAAAAAAGAAAAAAAGAAAAAAAGAAAAAAAG	534						
	551	ATTCCTTATTCCTCCAAAAAAAGAAAAAAAGAAAAAAAGAAAAAAAG	593						
RESULT	5								
BASE COUNT	201	a	138	c	154	g	195	t	ORIGIN
Query Match	63.3%		Score	338;	DB	9;	Length	688;	
Best Local Similarity	76.1%		Pred.	No.	1.7e-72;				
Matches	507;	Conservative	0;	Mismatches	0;	Indels	159;	Gaps	1;
Qy	28	GGCGGAGAGTAGGGAGGGGGTGTCCCGCCGGGGTGTCTATCGCTTCGCGA	87						
	13	GGCGGAGAGTAGGGAGGGGGTGTCCCGCCGGGGTGTCTATCGCTTCGCGA	72						
Qy	88	ACCTACTCAGCGCCAGCTGAGAAGAGTGAGGAGAAGTGTCTGCTGCGGTGTCGAGA	147						
	73	ACCTACTCAGCGCCAGCTGAGAAGAGTGAGGAGAAGTGTCTGCTGCGGTGTCGAGA	132						
Qy	148	CGCGGAGGAACTGCGAGCGAGAAATAACACGCCCTTCGCTTCAGTGTGAAGG	207						
	133	CGCGGAGGAACTGCGAGCGAGAAATAACACGCCCTTCGCTTCAGTGTGAAGG	192						
Qy	208	CCACGTGAAGATGCTGGCGGTG-----	229						
	193	CCACGTGAAGATGCTGGCGGTG-----	252						
Qy	230	-----	229						
	253	ACAAGCCCCCTGAAACCATATATGTATCACTGGAATTGAGTCACCGTTATCATGCC	312						
Qy	313	CATACCTTATATGACTGAGCTGATGATGATTATGAGTGTATTTGGCTTGCT	372						
Qy	230	-GATTTACACTGAGCTGAGAACAGTATGCTCATGCTATGTTGCTGTTGGACT	288						

	JOURNAL	Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
	REMARK	Sequence update by submitter
	COMMENT	On Sep 7, 2000 this sequence version replaced g1:6630855.
	FEATURES	Location/Qualifiers
QY	15 GTGAGGCCAGCAGGGCCAGAAGTAGGGAGGGGGCTCGCCCGGCGGGTGT 74	1. .434
Db	5 GGGAGGCCAGCAGGGCCAGAAGTAGGGAGGGGGCTCGCCCGGCGGGTGT 64	/organism="Homo sapiens" /db_xref="taxon:9606"
QY	75 ATGGCTTGCGAGAACCTCTCAGGACCGCAGTGGAGAGAGTGGAAAGTGC 134	/cell_line="U937" /note="From PHA stimulated cells"
Db	123 CTGGGTGCGAGAACCTCTCAGGACCGCAGTGGAGAGAGTGGAAAGTGC 182	1. .434
QY	195 TCACTGTAAGGCCACCTGAAGATGCTGCGGGTG----- 229	/gene="SKLF3" /note="TUCK" /product="chemokine-like factor 3" /protein_id="AAFI9600_1" /db_xref="GI:6630856" /translation="MDNWPKIKHRPFCFSVKGHVMLRLVALVAVCCLADGALIVRKLUFPNSGPYQKPVIEKEVL"
Db	243 TTTTATCATCGCACAGCCCCTGAACCCATAATGTTATCACTGGATTGAAGTCACCG 302	BASE COUNT ORIGIN 230 ----- 229
QY	303 TTACTTATTTCTACACTTTATGTTACTCAGACTTGATCGATTATGAAAGTTAT 362	Query Match 59.3%; Score 316.4; DB 9; Length 434; Best Local Similarity 81.3%; Pred. No. 3e-67; Mismatches 0; Indels 96; Gaps 1;
QY	230 -----GATTTATCAACTCAGCTGTAACACAGTATTCTCATGCTCATGTT 275	Matches 423; Conservative 0; Mismatches 1; Indels 96; Gaps 1;
Db	363 TTGGCCATTGCTGTGATTACACTGCACTGGTACAGTATTCTCATGCTCATGTT 422	QY 15 GTGAGGCCAGCAGGGCCAGAAGTAGGGAGGGGGCTCCCGGGGGTGTGTCTCCGCCGGGGTGGGGTGT 74
QY	276 CTGTTGCGACACTGATACCAAGAACACACATGACAGTGGTGGAGGGGGTGTGAC 335	11 GGGAGGCCAGCTGGCGAGAAGTAGGGAGGGGGCTCCCGGGGGTGTGTCTCCGCCGGGGTGGGGTGT 70
Db	423 CTGTTGCGACACTGATACCAAGAACACACATGACAGTGGTGGAGGGGGTGTGAC 482	75 ATCGTTGCGAGACCTACTCAGCAGCCAGCTGAGAAGTGGAAAGTGGCTG 134
QY	336 TTGAGACAGCAGATGCTGCTGGCCAGGGCCATTATGGCGAGTCCTGTTCA 395	71 ATCGTTGCGAGACCTACTCAGCAGCCAGCTGAGAAGTGGAAAGTGGCTG 130
Db	483 TTGTGACAGCAGTATGCTCTGCGAGGGGCCCTATTACCGGAGGCTCTTCA 542	QY 135 CTGGCTCTGAGACCCGATGATACAGTCAGGGAAATAAACATGCCCTCTGCT 194
QY	316 ATGCCAGGGCTCTTACCGAGAAAAGCCCTGTCATGAAAAAAGAGGTTGTAAATT 455	131 CTGGCTCTGAGACCCGATGATACAGTCAGGGAAATAAACATGCCCTCTGCT 190
Db	543 ATCCAGGGCTCTTACCGAGAAAAGCCCTGTCATGAAAAAAGAGGTTGTAAATT 602	QY 195 TCACTGTAAGGCCACCTGAAGATGCTCGGGCTGATATTATCACTCACTGTTACAA 254
QY	456 ATTTACTTTAGTTAGTAACTAAGTTAACATATTCGTATCTCCAAAAAAA 515	Db 191 TCACTGTAAGGCCACCTGAAGATGCTCGGGCTGATATTATCACTCACTGTTACAA 224
Db	603 ATTTACTTTAGTTAGTAACTAAGTTAACATATTCGTATCTCCAAAAAAA 662	QY 255 CAGTATCATGCTCATCGTATCTGTTGGACTCTGATACCGAGAACCCACAACATTACAG 314
QY	516 AAAAAA 522	Db 225 ----- 224
Db	663 AAAAAA 669	QY 315 TTGGTGGAGGGCTCTGTCATCCAGGGCTTACCGAGAACCTGTCAGAAA 434
RESULT 8	AI135381 AF135381 434 bp mRNA linear PRI 07-SEP-2000	Db 225 -----GGTGTGTTGCACTTGTCAGACAGCTGTCAGCTGCTGCGACGGGCCTTA 274
LOCUS	Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,	QY 375 TTACCGGAGACTCTCTGTCATCCAGGGCTTACCGAGAACCTGTCAGAAA 434
DEFINITION	alternatively spliced.	Db 275 TTACCGGAGACTCTCTGTCATCCAGGGCTTACCGAGAACCTGTCAGAAA 334
ACCESSION	AF135381	QY 435 AAAGGAAGTTGTAATTATATTACCTTTAGTTGATACAGTATTAAACATT 494
VERSION	AF135381.2 GI:9909693	Db 335 AAAGGAAGTTGTAATTATATTACCTTTAGTTGATACAGTATTAAACATT 394
KINNED WORDS		QY 495 TCTGTTCTCCAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 534
SOURCE	Homo sapiens	Db 395 TCTGTTCTCCAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 434
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	RESULT 9
REFERENCE	1 (bases 1 to 434)	G30204 LOCUS G30204 485 bp DNA linear SRS 05-OCT-1996
AUTHORS	Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D.	DEFINITION human STS SHGC-36487, sequence tagged site.
JOURNAL	Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China	ACCESSION G30204
REFERENCE	2 (bases 1 to 434)	VERSION G30204.1 GI:1593755
AUTHORS	Han,W.L.	KEYWORDS SRS; SIS sequence; primer; sequence tagged site.
TITLE	Direct Submission	

QY	6753	GGGAACCCGAGCCTGGCGAGAAGCTACTCAGGGAGCAGCTGAGAAGAGTGTGCTGCT	6694	Quality coverage: 4.6 in Q20 bases; agarose
Db	6693	ATCGCTTCGAGAACCTACTCAGGGAGCAGCTGAGAAGAGTGTGCTGCT	6634	-----
QY	135	CTGGGCTCTGAGACCGCATGATAACGTCAGCTGAGCAAACTGCSCCCTTCGT	194	* NOTE: This is a 'working draft' sequence. It
Db	6633	CTGGGCTCTGAGACCGATGATAACGTCAGCTGAGCAAACTGCSCCCTTCGT	6574	* consists of 18 contigs. The true order of
QY	. 195	TCACTGTGAAGGCCAGCTGAGATGCTGGCTTG	230	* is not known and their order in this sequence
Db	6573	TCAGCTGTGAAGGCCAGCTGAGATGCTGGCTTG	6538	* is arbitrary. Gaps between the contigs are repre-
QY	. * be preserved.	*****	*****	* runs of N, but the exact sizes of the gaps are not
Db	6573	TCAGCTGTGAAGGCCAGCTGAGATGCTGGCTTG	6538	* This record will be updated with the finished sequence as soon as it is available and the accession
RESULT	11			* is preserved.
AC018589/c				1. 1331: contig of 1331 bp in length
LOCUS	AC018589	Homo sapiens	151620 bp	1332 1431: gap of 100 bp in length
DEFINITION		clone RP11-13P4	DNA DRAFT	1432 2326: contig of 895 bp in length
VERSION	AC018589		SEQUENCE	2327 2426: gap of 100 bp
REFERENCE	AC018589.3	GI:7341919		2427 4519: contig of 2093 bp in length
AUTHORS	Birren, B., Linton, L., Nusbaum, C., and Lander, E.	HMG; HNGS_PHASE1; HTGS_DRAFT.		4520 4619: gap of 100 bp
TITLE	Homo sapiens			4620 6916: contig of 2297 bp in length
JOURNAL	Unpublished			6917 7016: gap of 100 bp
REFERENCE	2. (bases 1 to 151620)			7017 10850: contig of 3834 bp in length
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavskiy, L., Boukhalter, B., Brown, A., Burlett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearlano, K., Dewar, K., Domino, M., Doyle, M., Fenector, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, B., Hagos, B., Heatord, A., Hortsch, L., Karatas, A., Klein, J., Nowland, J.C., Johnson, R., Jones, C., Kann, J., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Menets, L., Morrow, J., Neylon, J., Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talanias, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M.		10851 10950: gap of 100 bp	
TITLE	Direct Submission			10951 15157: contig of 4207 bp in length
JOURNAL	Submitted (14-Dec-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA			15158 15257: gap of 100 bp
COMMENT	All Mar 30, 2000 this sequence version replaced gi:6692324.			15258 17752: contig of 2495 bp in length
Smit, A.F.A. & Green, P. (1996-1997)				17753 17852: gap of 100 bp
http://ftp.genome.washington.edu/RM/RepeatMasker.html				17853 22482: contig of 4630 bp in length
Center: Whitehead Institute/ MIT Center for Genome Research				22483 22582: gap of 100 bp
Center code: WIBR				22583 28540: contig of 3958 bp in length
Web site: http://www-seq.wi.mit.edu				26541 26640: gap of 100 bp
Contact: sequence_submissions@genome.wi.mit.edu				26641 30517: contig of 4277 bp in length
----- Project Information				30918 31017: gap of 100 bp
Center project name: 13379				31018 316401: contig of 5384 bp in length
Center clone name: 13_P_4				316402 36501: gap of 100 bp
Summary Statistics				36502 42254: contig of 5753 bp in length
Sequencing vector: M13; MT7815; 100% of reads				42255 42354: gap of 100 bp
Chemistry: Dye-terminator Big Dye; 100% of reads				42355 532974: contig of 10620 bp in length
Assembly program: phrap; version 0.960731				52975 53074: gap of 100 bp
Consensus quality: 141737 bases at least Q40				53075 62475: contig of 9401 bp in length
Consensus quality: 145736 bases at least Q30				62476 62575: gap of 100 bp
Consensus quality: 147339 bases at least Q20				62576 77661: contig of 10086 bp in length
Insert size: 149320; agarose-fp				72662 72761: gap of 100 bp
Insert size: 149320; sum-of-contigs				72762 889410: contig of 16649 bp in length
				89411 89510: gap of 100 bp
				89511 113391: contig of 23881 bp in length
				* 113392 113491: gap of 100 bp
				* 113492 115620: contig of 38129 bp in length
FEATURES				Location/Qualifiers
SOURCE				1. .151620 /organism="Homo sapiens"
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				/clone="RP11-13P4"
				/clone_id="RPC-11 Human Male BAC"
				1. .1331 /note="assembly_fragment"
				1432. .2326 /note="assembly_fragment"
				/clone_end?"7" /vector_end?"7"
				misc_feature
				2427. .4519 /note="assembly_fragment"
				10951. .15157 /note="assembly_fragment"
				15258. .17752 /note="assembly_fragment"
				15258. .17752 /note="assembly_fragment"
				17853. .22482 /note="assembly_fragment"
				17853. .22482 /note="assembly_fragment"
				22583. .26540 /note="assembly_fragment"
				22583. .26540 /note="assembly_fragment"
				26641. .30917 /note="assembly_fragment"

|||||||||||||||||||||||||||||||||||||||||
Db 147 ACGGGCCCTATTACCGAAGCTCTGTCATCCAGGGCTTACAGNAAGC 88
Qy 423 CTGTCAGAAAGAAAGAGTTGAAATTATTTACTTTAGTTGATACTAAGT 482
Db 87 CTGTCAGAAAGAAAGAGTTGAAATTATTTACTTTAGTTGATACTAAGT 28
Qy 483 ATTAACATATTCTGTATTCTCCA 508
Db 27 ATTAACATATTCTGTATTCTCCA 2

|||||||||||||||||||||||||||||||||||||
RESULT 14
AX330787/C AX330787 207 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 1:296 from Patent WO0194629.
DEFINITION AX330787
ACCESSION AX330787
VERSION AX330787.1 GI:18103765
KEYWORDS human
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL Patent: WO 0194629-A 1296 13-DEC-2001;
FEATURES Avalon Pharmaceuticals (US)
source /organism="Homo sapiens"
BASE COUNT 70 a 43 c 39 g 54 t 1 others
ORIGIN /db_xref="taxon:606" /db_xref="taxon:606"
1. .207
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/ab_xref="taxon:9606"
ORIGIN
Query Match 38.4%; Score 205; DB 6; Length 207;
Best Local Similarity 99.5%; Pred. No. 6.5e-40;
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 303 CAACATGACAGTGCTGGAGGGCTTGCACACTGTGACAGCAGTACGTGCTGCCG 362
Db 207 CAACATGACAGTGCTGGAGGGCTTGCACACTGTGACAGCAGTACGTGCTGCCG 148
Qy 363 ACGGGCCCTATTACCGAAGCTCTGTCATCCAGGGCTTACAGNAAGC 422
Db 147 ACGGGCCCTATTACCGAAGCTCTGTCATCCAGGGCTTACAGNAAGC 88
Qy 423 CTGTCATGAAAGAAAGAGTTGAAATTATTTACTTTAGTTGATACTAAGT 482
Db 87 CTGTCATGAAAGAAAGAGTTGAAATTATTTACTTTAGTTGATACTAAGT 28
Qy 483 ATTAACATATTCTGTATTCTCCA 508
Db 27 ATTAACATATTCTGTATTCTCCA 2

gene sets
Patent: WO 0194629-A 1517 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source /organism="Homo sapiens"
/ab_xref="taxon:606" /db_xref="taxon:606"
BASE COUNT 70 a 43 c 39 g 54 t 1 others
ORIGIN
Query Match 38.4%; Score 205; DB 6; Length 207;
Best Local Similarity 99.5%; Pred. No. 6.5e-40;
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 303 CAACATGACAGTGCTGGAGGGCTTGCACACTGTGACAGCAGTACGTGCTGCCG 362
Db 207 CAACATGACAGTGCTGGAGGGCTTGCACACTGTGACAGCAGTACGTGCTGCCG 148
Qy 363 ACGGGCCCTATTACCGAAGCTCTGTCATCCAGGGCTTACAGNAAGC 422
Db 147 ACGGGCCCTATTACCGAAGCTCTGTCATCCAGGGCTTACAGNAAGC 88
Qy 423 CTGTCATGAAAGAAAGAGTTGAAATTATTTACTTTAGTTGATACTAAGT 482
Db 87 CTGTCATGAAAGAAAGAGTTGAAATTATTTACTTTAGTTGATACTAAGT 28
Qy 483 ATTAACATATTCTGTATTCTCCA 508
Db 27 ATTAACATATTCTGTATTCTCCA 2

Search completed: June 25, 2003, 11:30:38
Job time : 1529 secs

RESULT 15
AX331008/C AX331008
DEFINITION Sequence 1:517 from Patent WO0194629.
ACCESSION AX331008
VERSION AX331008.1 GI:18121642
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrini; Hominoidea; Homo.
1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.,
Cancer gene determination and therapeutic screening using signature

OM nucleic - nucleic search, using sw model
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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description	
1	534	100.0	534	21	AAM38006	UCK-1 nucleotide s	
2	507	94.9	655	22	AAR44932	cDNA encoding novel	
C	3	498.2	93.3	538	22	AAB8515	Human EST-derived
C	4	498.2	93.3	538	22	AAB8548	Human EST-derived
5	497.2	93.1	558	22	AAH48335	Human colon cancer	
6	493.4	92.4	515	21	AAS7730	Human secreted pro-	
7	493.4	92.4	515	22	AAB64012	cDNA encoding human	
8	486.6	91.1	504	19	AAY59598	Human secreted pro-	
9	478.6	89.6	506	19	AAY59746	Human Secreted pro-	

ALIGNMENTS

XX	Example 4; Fig 1; 31bp; Chinese.
CC	This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis activity and a haemopoiesis stimulating effect. The invention relates to UCK proteins, their encoding nucleotide sequences and antibodies and antagonists against the proteins. The nucleotide and protein sequences are useful for the preparation of a composition for the diagnosis and treatment of diseases associated with abnormal immunocyte function and low haemopoiesis function caused by radiotherapy and chemotherapy used to treat tumours and other diseases.
CC	Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;
CC	Query Match 100.0%; score 534; DB 21; Length 534;
CC	Best Local Similarity 100.0%; Pred. No. 4.6e-107; Mismatches 0; Indels 0; Gaps 0; Matches 534; Conservative 0; Pairs 0; Mismatches 0; Indels 0; Gaps 0; XX
CC	1 GTCGCCCATCTGAGTGAAGCGAGCTGGGAGAGTAGGGAGGCGGTGCTGGCG 60
CC	1 GTCGCCATCTGAGTGAAGCGAGCTGGGAGAGTAGGGAGGCGGTGCTGGCG 60
CC	1 CGTGGCGGTCTATGCCTGCGAGAACCTACTCAGGACCCAGTGAGAGAGTGAG 120
CC	1 CGTGGCGGTCTATGCCTGCGAGAACCTACTCAGGACCCAGTGAGAGAGTGAG 120
CC	61 CGTGGGGTCTATGCCTGCGAGAACCTACTCAGGACCCAGTGAGAGAGTGAG 120
CC	61 CGTGGGGTCTATGCCTGCGAGAACCTACTCAGGACCCAGTGAGAGAGTGAG 120
CC	121 GCGAAGCTGCTGCGGGTGCAGCACGCCATGGATAACCTGCGCCGAATAACA 180
CC	121 GCGAAGCTGCTGCGGGTGCAGCACGCCATGGATAACCTGCGCCGAATAACA 180
CC	181 TGCCTCTCTGCTTCTGGTGAAGGCCAGCTGGAGATGCGCCGCTGGATATTCAA 240
CC	181 TGCCTCTCTGCTTCTGGTGAAGGCCAGCTGGAGATGCGCCGCTGGATATTCAA 240
CC	241 CTCACTGTTAACACAGTATCATGCCATGTTATGCTGGACTGATACAGAAC 300
CC	241 CTCACTGTTAACACAGTATCATGCCATGTTATGCTGGACTGATACAGAAC 300
CC	301 CACAACTGAGCTGGGGTGTGACTGTGAGGTTGACCTGAGCTGATGCTGCTTC 360
CC	301 CACAACTGAGCTGGGGTGTGACTGTGAGGTTGACCTGAGCTGATGCTGCTTC 360
CC	361 CGACGGGCCCTATTAACGGAGCTTCTCATCCCGGGCTTRACAGAAA 420
CC	361 CGACGGGCCCTATTAACGGAGCTTCTCATCCCGGGCTTRACAGAAA 420
CC	361 CGACGGGCCCTATTAACGGAGCTTCTCATCCCGGGCTTRACAGAAA 420
CC	421 GCTGTGCTGAAAGAGAGTTGTGTAATTAAATACTTTAGTTGATACTAA 480
CC	421 GCTGTGCTGAAAGAGAGTTGTGTAATTAAATACTTTAGTTGATACTAA 480
CC	481 GTTAAACATATTCTGATCTCCAAAAAAAGAGTTGTGATACTAA 534
CC	481 GTTAAACATATTCTGATCTCCAAAAAAAGAGTTGTGATACTAA 534
XX	RESULT 2
XX	AAS44932 standard; cDNA; 655 BP.
XX	AAS44932; 18-DEC-2001 (first entry)
XX	cDNA encoding novel human secretory protein, Seq ID No 13.
XX	Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haemopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amytrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; XX
XX	KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss; XX
XX	OS Homo sapiens.
XX	PN WO200166689-A2.
XX	PD 13-SEP-2001.
XX	PR 05-MAR-2001; 2001WO-US04942.
XX	PR 07-MAR-2000; 2000US-0519705.
XX	PR 19-MAY-2000; 2000US-057454.
XX	PR 17-JUN-2000; 2000US-059193.
XX	PR 14-JUL-2000; 2000US-061847.
XX	PR 19-SEP-2000; 2000US-065363.
XX	PR 20-OCT-2000; 2000US-0693267.
XX	PA (HYSE-) HYSEQ INC.
XX	PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P; Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX	WPI: 2001-589934/66.
XX	P-PSDB; AAU28032.
XX	PT Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
XX	DR
PS	Claim 1; SEQ ID NO 13; 107pp; English.
XX	The invention relates to novel isolated human secreted polypeptides (I) and poly nucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (I) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemoattractive activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies, and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, CC fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS44920-AAS45395 represent novel human secreted protein CC coding sequences of the invention.
XX	Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;
XX	Query Match 94.9%; score 507; DB 22; Length 655;
XX	Best Local Similarity 100.0%; Pred. No. 3.6e-101; Mismatches 0; Indels 0; Gaps 0; Matches 507; Conservative 0; Pairs 0; Mismatches 0; Indels 0; Gaps 0; XX
XX	19 AGCGAGCTGGGAGAGTAGGGAGGGGGCTCGCCGGGGTGCATCG

PT antibodies and research use -
 XX
 PS claim 1; Page 451; 1275pp; English.

QY |||||||
 Db 1 AGCCGAGCTGGCAGAAGTGGGGAGGGCGGTCTCCCGCGGTGGGGTCATCG 60
 QY 79 CTTCGGAGAACCTACTTCAGGCAGCGTCAAGAAGAGTTGGGAAGAGTCTGCTG 138
 Db 61 CTTCGCAGAACCTACTTCAGGCAGCGTCAAGAAGAGTTGGGAAGAGTCTGCTG 120
 QY 139 GCTCGAGACCGGAGTAACTGAGCAGCGGAATAAACATGCCCTCTCTCTCG 198
 Db 121 GCTCGAGACCGGATGATGATACGTCAGCGAGCGAAATAAACATGCCCTCTCTCG 180
 QY 199 TCTGAAGGCCAACCTGAAAGTGCTGGCGGCGATATTACAACCTACTGTAACACT 258
 Db 181 TGTGAARGGCCAACCTGAAAGTGCTGGCGGCGATATTACAACCTACTGTAACACT 240
 QY 259 ATTCATGCCATCGTGTGGCACATGATCAGAACACATTGAGCTGG 318
 Db 241 ATTCACTCATCGTGTGGCACATGATCAGAACACATTGAGCTGG 300
 QY 319 TGGAGGGTGTGACTGTGACAGCAGTATGCTGCTGCCGAGGGCCCTATTAA 378
 Db 301 TGGAGGGTGTGACTGTGACAGCAGTATGCTGCTGCCGAGGGCCCTATTAA 360
 QY 379 CCGGAACTCTGTCAAATCCAGGGTTTACAGAAAAGGCTGTGATGAAAAAA 438
 Db 361 CCGGAACTCTGTCAAATCCAGGGTTTACAGAAAAGGCTGTGATGAAAAAA 420
 QY 439 AGAAAGTTGPAATTATATACCTTTAGTTGATCAGAAGTTAACATATTCTG 498
 Db 421 AGAAAGTTGPAATTATATACCTTTAGTTGATCAGAAGTTAACATATTCTG 480
 QY 499 TATCTTCAAAAAAAGAAAAAA 525
 Db 481 TATCTTCAAAAAAAGAAAAAA 507

RESULT 3
 AAH9815/C
 ID AAH9815 standard; cDNA; 538 BP.
 XX
 AC AAH9815;
 AC
 XX
 DT 12-OCT-2001 (first entry)
 DE Human EST-derived coding sequence SEQ ID NO: 372.

KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.

OS Homo sapiens.

XX
 PN WO20154477-A2.

DD 02-AUG-2001.

XX
 PF 25-JAN-2001; 2001IWO-US02687.

PR 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.

XX
 PA (HYSEQ INC.

XX
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 Cao Y, Drmanac RA, Zhang J, Weruman T;
 XX
 DR WPI; 2001-476164/51.
 DR P-PSDB, AAM23856.

XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use -
 XX
 PS claim 1; Page 451; 1275pp; English.

QY The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.

CC Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

CC Query Match 93.3%; Score 498.2; DB 22; Length 538; Best Local Similarity 99.4%; Pred. No. 2.8e-99; Matches 500; Conservative: 0; Mismatches 3; Indels 0; Gaps 0;

CC QY 15 GTGAGGCCAGCTGGCGAGAAGTAGGGAGGGCGCTCGCCGGGGTGTCTGCT 74
 Db 503 GGGAGCCAGCTGGCGAGAAGTAGGGAGGGCGCTCGCCGGGGTGTCTGCT 444
 QY 75 ATCCCTTCCAGAACCTACTCAGGCCAGCAGCAGGAGAGTTGAAGGAAGTGTCTG 134
 Db 443 ATCGCTTCGAGAACCTACTCAGGCCAGCAGTGGCTG 384
 QY 135 CTGGCTTCAGGCCAGGATGATGAACTGCGACGGCGCTTGCT 194
 Db 383 CTGGCTTCAGGCCAGGATGATGAACTGCGACGGCGCTTGCT 324
 QY 195 TCAGTGTGAAGGCCACGTGAAGATGCTCCGGCTGGTATACACTACAGTGTACAA 254
 Db 263 CAGTATCTGCTCATCGTGTGGACTGTACAGAACCTGACAG 204
 QY 315 TTGGGGAGGGCTTGTGACTGTGACAGCATATGCTGCTGCGACGGGCCCTA 374
 Db 203 TTGGGGAGGGCTTGTGACTGTGACAGCATATGCTGCTGCGACGGGCCCTA 144
 QY 375 TTACGGAGCTCTGTCATCCAGGGCTTACCGAAAACCTGTCATGAA 434
 Db 143 TTACGGAGCTCTGTCATCCAGGGCTTACCGAAAACCTGTCATGAA 84
 QY 435 AAAAGGAAGTTGTAATTATATACCTTTAGTTGATACATAAGTAAACATT 494
 Db 83 AAAAGGAAGTTGTAATTATACCTTTAGTTGATACATAAGTAAACATT 24
 QY 495 TCTGATCTCCAAAAAA 517
 Db 23 TCTGATCTCCAAAAAA 1

RESULT 4
 AAH98548/C
 ID AAH98548 standard; cDNA; 538 BP.
 XX
 AC AAH98548;
 XX
 DT 12-OCT-2001 (first entry)
 DE Human EST-derived coding sequence SEQ ID NO: 405.

XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.

XX
 OS Homo sapiens.

XX

	Db	23	TCTGATTCCTAAAAAA	1
PN XX			WO200154477-A2.	
PD 02-AUG-2001.				
XX				
PF 25-JAN-2001; 2001WO-US02687.				
XX				
PR 25-JAN-2000; 2000US-0491404.	RESULT	5	AHH34835	
PR 17-JUL-2000; 2000US-0617746.	ID		AAH4835 standard; cDNA; 558 BP.	
PR 03-AUG-2000; 2000US-0631451.	XX			
PR 15-SEP-2000; 2000US-0663870.	AC		AAH34835;	
XX	XX			
PA (HYSE-) HYSEQ INC.	DT	03-SEP-2001	(first entry)	
XX	XX			
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;	DE		Human colon cancer antigen encoding cDNA. SEQ ID NO:1917.	
PT Cao Y, Drmanac RA, Zhang J, Wernham T;	XX			
XX	KW		human; colon cancer; colon cancer antigen; diagnosis; detection;	
DR WPI; 2001-476164-51.	XX		colonctal carcinoma; ss.	
P-PSDB; AAM23889.	OS		Homo sapiens.	
XX	XX			
PT Isolated polypeptide for treatment of diseases, diagnostics, raising	PN		WO200122920-A2.	
PT antibodies and research use -	XX			
XX	PD	05-APR-2001.		
PS Claim 1; Page 467; 1275pp; English.	XX			
XX	XX			
CC The present invention provides the protein and coding sequences of novel	PR	29-SEP-1999;	99US-0137137.	
CC proteins from a variety of organisms, including human, dog, cat, horse,	PR	03-NOV-1999;	99US-0163280.	
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea	XX			
CC urchin and tomato. These were derived from expressed sequence tags (ESTS).	PA		(HUMA-) HUMAN GENOME SCI INC.	
CC forensics, gene mapping, identification of mutations, to assess	XX			
CC biodiversity and for nutritional purposes. The present sequence is a cDNA	PI		Ruben SM, Barash SC, Birse CE, Rosen CA;	
CC of the invention.	XX			
XX	DR			
Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;	DR			
PS Query Match Best Local Similarity 99.4%; Score 498.2; DB 22; Length 538;	XX			
PS Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	PT		Nucleic acids encoding 4277 human colon cancer-associated polypeptides useful for preventing, diagnosing and/or treating colorectal cancers	
QY 15 GTGAAGCCGAGCTGGGGAGAAGTAGGGAGGGGGCTCGCGCCCGGTTGGGTGCT 74	XX			
DB 503 GCGAAGCCGAGCTGGGGAGAAGTAGGGAGGGGGCTCGCGCCCGGTTGGGTGCT 444	PS		Claim 1; Page 3428; 9803pp; English.	
QY 75 ATGGCTCTGCAGACCTACTCAGGCCAGCTGAGAGACTGTAGGGAAAGTGCTGCTG 134	XX			
DB 443 ATGGCTCTGCAGACCTACTCAGGCCAGCTGAGAGACTGTAGGGAAAGTGCTGCTG 384	CC		AHH2943 to AAH37195 and AAC73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patient's own production of P.	
QY 135 CCGGGCTGCGACGGCATGGATAAGTGCGCCGCGTGGATTAACATCGCCCTCTGCT 194	CC		Additionally, N may be used to produce the colon cancer-associated P, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAC73196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the present invention.	
DB 383 CCGGGCTGCGACGGCATGGATAACGTGCACGCCGAAATAAACATCGCCCTCTGCT 324	CC		N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID No:1027 to 1052, 7921 and 7922.	
QY 195 TCACTGCTGAAAGCCACGGTGAAGATGCTGCCGTGGATTAACACTACTGTAACAA 254	XX			
DB 323 TCACTGCTGAAAGCCACGGTGAAGATGCTGCCGTGGATTAACACTACTGTAACAA 264	CC			
QY 255 CAGTATTCATGCTCATGTAATGCTGTTGGACTGATACCAGAACACACATGACAG 314	CC			
DB 263 CAGTATTCATGTCATGCTCATGTAATGCTGTTGGACTGATACCAGAACACATGACAG 204	CC			
QY 315 TGGTGGAGGGGTGTTGACTGTGACASAGTAGTGCTGCTGGAGGGGACCTRA 374	XX			
DB 203 TGGTGGAGGGGTGTTGACTGTGACAGCATGCTGCTGGAGGGGACCTRA 144	SQ		Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;	
QY 375 TTGACCGAACCTCTGCTCATCCAGGGCTCTACAGAAAGCCCTGCTGATGAA 434	Query Match Best Local Similarity 98.4%; Score 497.2; DB 22; Length 558;			
DB 143 TTGACCGAACCTCTGCTCATCCAGGGCTCTACAGAAAGCCCTGCTGATGAA 84	PS Matches 499; Conservative 2; Mismatches 6; Indels 0; Gaps 0;			
QY 435 AAAAGAGTTGTAATTATATCTTTAGTTGACTAGTAACTATATT 494	QY 16 TGAAGCCGAGCTGGGGAGAAGTAGGGAGGGGGCTCCCGGGGGTGGCTGCTGCTA 75			
DB 83 AAAAGAGTTGTAATTATATCTTTAGTTGACTAGTAACTATATT 24	DB 11 TGAAGYSSGAGCTGGAGAAGTAGGGAGGGGGCTCCCGGGGGTGGCTGCTGCTA 70			
QY 495 TCTGATTCCTCAAARAAA 517	QY 76 TCGCTCGAGAACCTACTCAGGCCAGCTGGAGAGTGTAGGGAAAGTGCTGCTGCTG 135			
	DB 71 TCGCTCGAGAACCTACTCAGGCCAGCTGGAGAGTGTAGGGAAAGTGCTGCTGCTG 130			

QY	Db	136 TGGGCTCGAGACCGGATGATAACGGCAGAACAACTGGAGCCAAATAAACATCGCCCTCTGCTT 195
QY	Db	131 TGGGCTCGAGACGCCAGGATAACGTGCAAGCCAAATAAACATCGCCCTCTGCTT 190
QY	Db	196 CAGTGTGAAGGCCAGCTGAGAGCTCGGGCTGAGATAACTGACTGAACTGACAC 255
QY	Db	191 CAGTGTGAAGGCCAGCTGAGAGCTCGGGCTGAGATAACTGACTGAACTGACAC 250
QY	Db	256 AGTATTCTCATCTGATCTGCTGCACTGATACAGAACACATGACAG 315
QY	Db	251 AGTATTCTCATCTGATCTGCTGCACTGATACAGAACACATGACAG 310
QY	Db	316 TGGGAGGGGTGTTGACTGTGACAGAGTAGTGCTCTTGCCAGGGGCCCTAT 375
QY	Db	311 TGGGAGGGGTGTTGACTGTGACAGAGTAGTGCTCTTGCCAGGGGCCCTAT 370
QY	Db	376 TTACGGGAACTTCAGTCATCCAGCGGTCCATTACCGAARAAAGCCGTCAGAAA 435
QY	Db	371 TTACGGGAACTTCAGTCATCCAGCGGTCCATTACCGAARAAAGCCGTCAGAAA 430
RESULT 6		
QY	Db	436 AAAAGAGTTGTAATTATATTCTTTAGTTGACTAAGTAACATATT 495
QY	Db	431 AAAGAAGTTGTAATTATATTCTTTAGTTGACTAAGTAACATATT 490
QY	Db	496 CTGATCTCCAAAAAAANAAA 522
QY	Db	491 CTGATCTCCAAAAAAANAAA 517
ID	AAA87730	standard; cDNA; 515 BP.
XX		
AC		
XX		
DT	28-NOV-2000	(first entry)
XX		
DE	Human secreted protein encoding cDNA	SEQ ID #29.
XX		
KW	Human; secreted protein; forensic procedure; gene therapy;	
KW	chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;	
KW	cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;	
KW	brain disorder; skeletal muscle disorder; eye disorder; obesity;	
KW	mitochondriopathy; diabetes; atherosclerosis; Alzheimer's disease;	
KW	neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;	
KW	septic shock; impotence; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO20037491-A2.	
XX		
PD	29-JUN-2000.	
XX		
PF	20-DESC-1999;	99WO-IB02058.
XX		
PR	22-DEC-1998;	980S-0113686.
XX		
PR	25-JUN-1999;	99US-0141032.
XX		
PA	(GEST) GENSET.	
XX		
PI	Bougueret L, Dumas J, Duclert A;	
XX		
DR	WPI; 2000-442637/38.	
DR	P-PSDB; AAB25768.	
PT	Poly nucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome mapping procedures -	
PT	Claim 1; Page 169-170; 30pp; English.	
CC	This sequence represents human cDNA encoding a secreted protein. The invention relates to sequences AAA87725-A87774 which encode human	
CC	secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochrondriopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.	
CC	Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;	
Query Match		92.4 %; Score 493.4; DB 21; Length 515;
Best Local Similarity		99.4%; Pred. No. 3.1e-98;
Matches		505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Db		SQ
QY	15 GTGAGCCGAGCTGGCGAGAACTCAGCGACAGTGAGAAGGTGAGGAAGTGTGCT 74	
Db	8 GGAGGCCAGCTGGCGAGAACTCAGCGACAGTGAGAAGGTGAGGAAGTGTGCT 66	
QY	75 ATCCTTCAGCACGAACTACTCAGCAGCGAGTAGGGAGCCGGCTCCCGGGTGGCTCG-CGGGGTGGNGTGTG 134	
Db	67 ATCGCTTCAGCACGAACTACTCAGCAGCGAGTAGGGAGCCGGCTCCCGGGTGGCTCG-CGGGGTGGNGTGTG 126	
Db	135 CTGGGTCTCGCAGACGGATGATGAGAACGGCAAATAAACATCGCCCCCTTCNGCT 194	
Db	127 CTGGGTCTCGCAGACGGATGATGAGAACGGCAAATAAACATCGCCCCCTTCNGCT 186	
QY	195 TCACTGTGAAGGCCACGGTAAAGATGCTGCGGGTGGATTATCAACTCAGCTGTAACAA 254	
Db	187 TCACTGTGAAGGCCACGGTAAAGATGCTGCGGGTGGATTATCAACTCAGCTGTAACAA 246	
QY	255 CAGTATTCTCATCTGATCTGATGAGAACGGCAAATAAACATCGCCCCCTTCNGCT 314	
Db	247 CAGTATTCTCATCTGATCTGATGAGAACGGCAAATAAACATCGCCCCCTTCNGCT 306	
QY	315 TTGGTGGAGGGTGTGCACTGTGATGAGAACGGCAAATAAACATCGCCCCCTTCNGCT 374	
Db	307 TTGGTGGAGGGTGTGCACTGTGATGAGAACGGCAAATAAACATCGCCCCCTTCNGCT 366	
QY	375 TTACGGGAGCTCTGTCACACCGGTCTTACCGAAAAGGCTGTCATGAAA 434	
Db	367 TTACGGGAGCTCTGTCACACCGGTCTTACCGAAAAGGCTGTCATGAAA 426	
QY	435 AAAAGAGTTGTAATTATATTACTTTAGTTGACTAAGTTAACATATT 494	
Db	427 AAAAGAGTTGTAATTATATTACTTTAGTTGACTAAGTTAACATATT 486	
QY	495 TCTGTTCTCCAAAAAAANAAA 522	
Db	487 TCTGTTCTCCAAAAAAANAAA 514	
RESULT 7		
DR	AAF64012	
ID	AAF64012	standard; cDNA; 515 BP.
XX		
AC	AAF64012;	
XX		
DT	05-APR-2001	(first entry)
XX		
DE	cDNA encoding human secreted protein #13.	
XX		
KW	Secreted protein; prevention; treatment; diagnosis; disease; infection; ds.	

XX
OS Homo sapiens.
XX
PN WO200100806-A2.
XX
PD 04-JAN-2001.
XX
PF 21-JUN-2000; 2000W0-IB00951.
XX
PR 25-JUN-1999; 99US-0141032.
XX
PR 21-DEC-1999; 99US-0469099.
XX
(GBST) GENSET.
XX
Dumas Mline Edwards J, Bouqueleret L, Jobert S;
XX
DR; WPI; 2001-071487/08.
XX
PT 49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples -
XX
PS Claim 1; Page 225; 307PP; English.
XX
CC The present invention relates to 49 Secreted proteins and the cDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
SQ Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;
Query Match Best Local Similarity 99.4%; Score 493.4; DB 2/2; Length 515;
Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 15 GTCAGAAGCGAGGTGGCGAGAGTAGGGGAGGGGGCTGCTCG -CGGGGGCGCTGC 66
DB 8 GGAGAGCGAGCTGGGGAGAGTAGGGGAGGGGGCTGCTGC 74
OY 75 ATGGCTTGCGAGAACCTACTCAGGGCACCTGAGAAAGTGGAGGAAAGTGTCTGCTG 134
DB 67 ATGCTTGCGAGAACCTACTCAGGGCACCTGAGAAAGTGGAGGAAAGTGTCTGCTG 126
OY 135 CCGGGTTCAGACGGGAGGATAAGTGGAGGGAAATAAACATGGCCCTCTGCT 194
DB 127 CGGGGCTGCAAGACGGGATGATAAGTGGAGGGAAATAAACATGGCCCTCTGCT 186
OY 195 TCAGTGTGAAGGCCACGGTGAAGATGCTGGCGCTGATATTATCACTACTACTGGTAACAA 254
DB 187 TCACTGTGAAGGCCACGGTGAAGATGCTGGCGCTGATATTATCACTACTGTGTAACAA 246
OY 255 CAGTATTCATGCTCATGTACTGTGTTGCACTCATACGAGAAACACACATGTGACAG 314
DB 247 CAGTATTCATGCTCATGTACTGTGTTGCACTGTGACAGAAACACACATGTGACAG 306
OY 315 TTGGTGAGGGGTGTTGCACTGTGACAGAAACACACATGTGACAG 374
DB 307 TTGGTGAGGGGTGTTGCACTGTGACAGAAACACACATGTGACAG 366
OY 375 TTACCGGAAGCTCTGTCATCCAGGCTCTTACCAAGAAAAGCCTGTGCACTGAA 434
DB 367 TTACCGGAAGCTCTGTCATCCAGGCTCTTACCAAGAAAAGCCTGTGCACTGAA 426
OY 435 AAAAGAGAGTGTATTTATTTACTTTTACTAAGTTAACATAT 494
DB 427 AAAAGAGAGTTGTATTTATTTACTTTTACTGTTAACATAT 486
OY 495 TCTGTATTCACAAAAAA 522
DB 487 TCTGTATTCACAAAAAA 514

XX
OS Homo sapiens.
XX
PN WO9839448-A2.
XX
PD 11-SRP-1998.
XX
PP 06-MAR-1998; 98WO-US04493.
XX
PR 02-OCT-1997; 97US-0061060.
XX
PR 07-MAR-1997; 97US-0038621.
XX
PR 07-MAR-1997; 97US-004161.
XX
PR 07-MAR-1997; 97US-004162.
XX
PR 07-MAR-1997; 97US-004163.
XX
PR 07-MAR-1997; 97US-004333.
XX
PR 07-MAR-1997; 97US-004334.
XX
PR 07-MAR-1997; 97US-004336.
XX
PR 07-MAR-1997; 97US-004337.
XX
PR 11-APR-1997; 97US-0043311.
XX
PR 11-APR-1997; 97US-0043312.
XX
PR 11-APR-1997; 97US-0043313.
XX
PR 11-APR-1997; 97US-0043314.
XX
PR 11-APR-1997; 97US-0043348.
XX
PR 11-APR-1997; 97US-00433568.
XX
PR 11-APR-1997; 97US-00433569.
XX
PR 11-APR-1997; 97US-00433576.
XX
PR 11-APR-1997; 97US-00433578.
XX
PR 11-APR-1997; 97US-00433580.
XX
PR 11-APR-1997; 97US-00433669.
XX
PR 11-APR-1997; 97US-00433670.
XX
PR 11-APR-1997; 97US-00433671.
XX
PR 11-APR-1997; 97US-00433672.
XX
PR 11-APR-1997; 97US-0043674.
XX
PR 23-MAY-1997; 97US-004367492.
XX
PR 23-MAY-1997; 97US-0044500.
XX
PR 23-MAY-1997; 97US-0044501.
XX
PR 23-MAY-1997; 97US-0044502.
XX
PR 23-MAY-1997; 97US-0044503.
XX
PR 23-MAY-1997; 97US-0044581.
XX
PR 23-MAY-1997; 97US-0044582.
XX
PR 23-MAY-1997; 97US-0044583.
XX
PR 23-MAY-1997; 97US-0044584.
XX
PR 23-MAY-1997; 97US-0044585.
XX
PR 23-MAY-1997; 97US-0044586.
XX
PR 23-MAY-1997; 97US-0044587.
XX
PR 23-MAY-1997; 97US-0044588.
XX
PR 23-MAY-1997; 97US-0044589.
XX
PR 23-MAY-1997; 97US-0044590.
XX
PR 23-MAY-1997; 97US-0044592.
XX
PR 23-MAY-1997; 97US-0044593.
XX
PR 23-MAY-1997; 97US-0044594.
XX
PR 23-MAY-1997; 97US-0044595.
XX
PR 23-MAY-1997; 97US-0044596.
XX
PR 23-MAY-1997; 97US-0044597.
XX
PR 23-MAY-1997; 97US-0044598.
XX
PR 23-MAY-1997; 97US-0044599.
XX
PR 23-MAY-1997; 97US-0044600.

PR 23-MAY-1997; 97US-0047613. CC
 PR 23-MAY-1997; 97US-0047614. CC
 PR 23-MAY-1997; 97US-0047615. CC
 PR 23-MAY-1997; 97US-0047617. CC
 PR 23-MAY-1997; 97US-0047618. CC
 PR 23-MAY-1997; 97US-0047632. CC
 PR 23-MAY-1997; 97US-0047633. CC
 PR 06-JUN-1997; 97US-0048964. CC
 PR 13-JUN-1997; 97US-0049610. CC
 PR 08-JUL-1997; 97US-0051926. XX
 PR 16-JUL-1997; 97US-0052874. XX
 PR 18-AUG-1997; 97US-0055724. XX
 PR 22-AUG-1997; 97US-0056630. XX
 PR 22-AUG-1997; 97US-0056631. XX
 PR 22-AUG-1997; 97US-0056632. XX
 PR 22-AUG-1997; 97US-0056636. XX
 PR 22-AUG-1997; 97US-0056637. XX
 PR 22-AUG-1997; 97US-0056652. XX
 PR 22-AUG-1997; 97US-0056654. XX
 PR 22-AUG-1997; 97US-0056845. XX
 PR 22-AUG-1997; 97US-0056862. XX
 PR 22-AUG-1997; 97US-0056864. XX
 PR 22-AUG-1997; 97US-0056872. XX
 PR 22-AUG-1997; 97US-0056874. XX
 PR 22-AUG-1997; 97US-0056875. XX
 PR 22-AUG-1997; 97US-0056876. XX
 PR 22-AUG-1997; 97US-0056877. XX
 PR 22-AUG-1997; 97US-0056878. XX
 PR 22-AUG-1997; 97US-0056879. XX
 PR 22-AUG-1997; 97US-0056880. XX
 PR 22-AUG-1997; 97US-0056882. XX
 PR 22-AUG-1997; 97US-0056884. XX
 PR 22-AUG-1997; 97US-0056885. XX
 PR 22-AUG-1997; 97US-0056886. XX
 PR 22-AUG-1997; 97US-0056889. XX
 PR 22-AUG-1997; 97US-0056892. XX
 PR 22-AUG-1997; 97US-0056893. XX
 PR 22-AUG-1997; 97US-0056894. XX
 PR 22-AUG-1997; 97US-0056903. XX
 PR 22-AUG-1997; 97US-0056908. XX
 PR 22-AUG-1997; 97US-0056909. XX
 PR 22-AUG-1997; 97US-0056910. XX
 PR 22-AUG-1997; 97US-0056911. XX
 PR 05-SEP-1997; 97US-0057650. XX
 PR 05-SEP-1997; 97US-0057659. XX
 PR 05-SEP-1997; 97US-0057761. XX
 PR 12-SEP-1997; 97US-0058785. XX
 PA (HUMA-) HUMAN GENOME SCI INC. XX
 PT Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA; Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS; KW Ily Y, Moore PA, Ni J, Olsen HS, Rosen CA; Ruben SM, Shl Y, Soppet DR, Young PE, Yu Gu, Zeng Z; XX DR WPI: 1998-506364/43. DR P-PSDB; AAW7816.

XX New isolated human genes and the secreted polypeptide(s) they encode PT - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders XX Claim 1; Page 320; 721pp; English.

XX This sequence represents a nucleic acid molecule designated Gene 88 from the human cDNA clone HAUAV32 (deposited as clone ATCC 97901 and ATCC 209047) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV5502) for increasing the stability of

CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-v59812; amino acid sequences AAW74731-WW5026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).
 CC (see AAV59511 for described uses).

XX Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other:
 Query Match 91.1%; Score 486.6; DB 19; Length 504;
 Best Local Similarity 99.0%; Pred No. 9.4e-97;
 Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 CC
 QY 21 CCGACGCTGGCGAGAGTAGGGAGGGAGGGCGGTGCGCAGCGGGTGTGCTATGCCT 80
 Db 1 CCGACGCTGGCGAGAGTAGGGAGGG-ACGAGCCGCCGGGG-ACGAGCCGCCGGGG-TCGCT 59
 QY 81 TCGCAGAACCTACTAGGAGCCACCTAGGAGAAAGTTAGGGAGAGTGCTGCGCTGCGCTGGT 140
 Db 120 CTGCGAGACGCATGAGATAAGTCGCGCAGAACATCSCCTCTGCGCTACTG 179
 QY 201 TGAAGGCCAGCTGAGATGCTGCCCTGGATATTATCACTCACTCTGGTACACAGTAT 260
 Db 180 TGAAGGCCAGTGAGATGCTGCCCTGGATATTATCACTCACTCTGGTACACAGTAT 239
 QY 261 TCATGCTCATGTAATGCTGTTGACTGATACCAGAACACACATGACAGCTGG 320
 Db 240 TCATGCTCATGTAATGCTGTTGACTGATACCAGAACACACATGACAGCTGG 299
 QY 321 GAGGGGTGTTCACTGTGACAGCAGTACCTGCTGCGACGGGCCCTTATTAC 380
 Db 300 GAGGGGTGTTGACTGTGACAGCAGTATCTGCTGCGACGGGCCCTTATTAC 359
 QY 381 GAAAGCTCTGTCATCCAGCGGCCCTTACACAGAAAAGCTTGATGAAAGAAC 440
 Db 360 GGAGCTCTGTCATCCAGCGGCCCTTACACAGAAAAGCTTGATGAAAGAAC 419
 QY 441 AAGTTGTTGTAATTTATATTACTTTTGTAGTGTAGTAATGTTAACATATTCTGTA 500
 Db 420 AAGTTGTTGTAATTTATATTACTTTTGTAGTGTAGTAATGTTAACATATTCTGTA 479
 QY 501 TTCTTCCAAAAAAAGAAAAAAAG 525
 Db 480 TTCTTCCAAAAAAAGAAAAAAAG 504

XX RESULT 9
 XX DE Human secreted protein gene 88 clone HAUAV32.
 XX ID AAV59746 standard; DNA; 506 BP.
 XX AC AAV59746;
 XX DT 19-JAN-1999 (first entry)
 XX DE Human secreted protein gene 88 clone HAUAV32.
 XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy; KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia; developmental abnormality; foetal deficiency; blood; allergy; renal; os; KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; KW cognitive disorder; schizophrenia; prostate; obesity; osteoporosis; thymus; KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

PS	Example 28; Page 173-174; 307pp; English.
XX	
AAXY7813-X97906	represent extended cDNA's which encode novel human secreted proteins (see AAY5612&Y3622) and which have cytostatic, thrombotic and osteoprotective activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.
CC	Sequence 500 BP; 135 A; 102 C; 125 G; 129 T; 9 other;
CC	Query Match 87.4%; Score 466.8; DB 20; Length 500;
CC	Best Local Similarity 98.8%; Pred. No. 1.9e-92;
CC	Matches 488; Conservative 4; Mismatches 5; Indels 2; Gaps 2;
CC	Db 2 GACGTGNNNSAGTAGGGAAAGCGGGCTCTGTCA 301
QY	23 GACGTGGCGAGGAGTAGGGAGGGGGGGGG-TTGTATCCTT 81
QY	337 TGTGACAGGAGTATGCCGCTCTGCCGACGGGCCTATTACCGGAACCTCTGTCA 396
QY	302 TGTGACASCGATGATGCTGCTTEGCCGAGGGGCCCTATTACGGAAACGCTCTGTCA 361
QY	397 TCCGAGCGGCCTTACAGAAAAGGCCCTGTCAAGAAMAAAAGAGTTTGATA 456
QY	362 TCCGAGCGGCCTTACAGAAAAGGCCCTGTCAAGAAMAAAAGAGTTTGATA 421
QY	457 TATTAATTTTGTGACTAATGTTAAACATATTTGTATTCCTTCACAAAAAAA 516
QY	422 TATTAATTTGTGACTAATGTTAAACATATTTGTGATTTCCACAAAAAAA 481
QY	517 AAAAAGAAAAAAA 533
QY	482 AAAAAGAAAAAAA 498
XX	RESULT 10
XX	AAX97826 standard; cDNA: 500 BP.
AC	23-SEP-1999 (first entry)
AC	Human secreted protein encoding cDNA #14.
KW	Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic; diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
KW	Homo sapiens.
OS	W09925825-A2.
XX	27-MAY-1999.
XX	13-NOV-1998; 98WO-1B01862.
PR	04-SEP-1998; 98US-0093273.
PR	13-NOV-1997; 97US-0066677.
PR	17-DEC-1997; 97US-0069557.
PR	09-FEB-1998; 98US-007121.
PR	13-APR-1998; 98US-0081563.
PR	10-AUG-1998; 98US-0096116.
PA	(GEST) GENSET.
XX	Bouquerel L, Ducleir A, Dumas Milne Edwards J;
XX	WPI; 1999 347472/29.
XX	P-PSB; AAY36142.
PT	Extended cDNAs encoding secreted proteins

The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK36232 represent the cDNA sequences of the invention that encode for novel human secreted proteins.

Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;

Query Match 79.6%; Score 425; DB 24; Length 439; Best Local Similarity 99.8%; Pred. No. 2. 3e-83; Min. Sim. 0.791

Matches 436; Conservative 0; Mismatches 0; Insertions 1; Deletions 1; Gaps 0; Total length 72 GCTATCGTTTCGAGAACCTACTCTAGGGAGCCAGCTGAGAAAGTGTAGGGAAAGTCCTG 131

Db
1 GCTATCGCTTCGCAAGAACCTACTCAGGGCAGCCAGCTGAGAAGAGITGAGGGAAAGTCG 60

QY
 132 CTGGCTGGGCTGCAGAGCGATGATAACGTGAGCCGAATATAACATGCCCTCT 191
 131 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| 130
 130 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 131 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 132 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db
121 GCTTCAGTGTGAAAGGCCACGTGAAAGATGCTCGGGTGGATATTATCAACTCACTGGTAA 180

DB
181 CAAAGAATTCATGCTATGTAACGTTGCACTGTGACAGCAGTAGCTGCTGGCGACGGGGCC 371
312 CAGTTGGTGGGGGGTTGACTGTGACAGCAGTAGCTGCTGGCGACGGGGCC 371
QY

Db
241 CAGTGGTGGGGGTGTTGCACCTGTGACAGCAGTATGCTCTGCCGACGGGGCC 300

QY
372 TTTATTACCGGAAGCTCTGTGTCATCCCGACGGTCTTACAGAAAAGSCTGTGCA 431

D _b	O _v
301 TTATTACCGGAAGCTCTGTCATCCCAAGGGCTTACAGAAAAGCTGTGCATG	360
432 AAAAAAAGAAGTTGTAATTATATTAATCTTATGTT-GATACTAAGTAAACA	490

Db 361 AAAAAAGAAGTTGTAATTATATTCTTGTGGATACTAAGTATAACA 420

Qy 491 TATTCTGATTCTCC 507
|||||

Db 421 TATTCTGTATTCTTCC 437

RESULT 13
AJM97873

XX LU AAXY9/8/3 Standard; CDNA; 413 bp.
AC AAXY97873;

XX
DT
XX
23-SEP-1999 (first entry)

DE Human secreted protein encoding cDNA #61.
XX

KW secreted protein; human; cytostatic; thrombotic; osteopatric; Lorieus;
KW diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
XX

OS
XX
Homo sapiens.

DE Human secreted protein 5' EST, SEQ ID NO: 145.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss;
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000BP-0200610.
 XX PR 26 FEB-1999; 99US-0122487.
 XX PA (GST) GENSET.
 XX PT Dumas Mine Edwards J, Duclert A, Giordano J;
 DR WPI; 2000-500381/45.
 XX P-PSDB; AAG00141.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5',ss and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1; SEQ ID 145; 71PP + CD-ROM; English.

CC The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
 XX Sequence 415 BP; 101 A; 97 C; 126 G; 91 T; 0 other;

Query Match 75.9%; Score 405.4; DB 21; Length 415;
 Best Local Similarity 99.8%; Pred. No. 4.2e-79; Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 15 CTGAAGGCCGACCTGGCGAGAGTAGGGAGGGGGGTGCCTCGCGCGCGGGCGCTGGT 74
 Db 9 GGGAAAGCCGAGCTGGCGAGAGTAGGGAGGGCGCTGGCGCGCGCGGGCGCTGGT 68
 OY 75 ATGGCTTCGCAGCGGATAGATAACGGAGCAGCTGGAGAAGACTGGAGGAAGTGCTGCG 134
 Db 69 ATGGCTTCGCAGCGGATAGATAACGGAGCAGCTGGAGAAGTGCTGCG 128
 OY 135 CTGGGCTCGAGAGACCTACTAGGGAGCTGGAGAAGTGCTGCG 194
 Db 129 CTGGGCTCGAGAGACCTACTAGGGAGCTGGAGAAGTGCTGCG 188
 OY 195 TCACTGAGAAGGCCAACGTTGAGATATTAACTCTACTGTTAC 254
 Db 189 TCAGTGTGAAAGGCCAACGTTGAGATATTAACTCTACTGTTAC 248
 OY 255 CAGTATCTCTCTCATGTTCTGTTGCACTGATACAGAACACACATGAG 314
 OY 249 CAGTATCTCTCATGTTCTGTTGCACTGATACAGAACACACATGAG 308
 OY 315 TTGGTGGAGGGGTGTTGCACTTGTGACGACGAGTGTGCTCT 374
 Db 309 TTGGTGGAGGGGTGTTGCACTTGTGACGACGAGTGTGCTCT 368

OY 375 TTACCGGAAGCTTCTGTCATCCAGGGTCTTACCGAAAAG 421
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 369 TTACCGGAAGCTTCTGTCATCCAGGGTCTTACCGAAAAG 415
 RESULT 15
 AAZ34051 AAZ34051 standard; cDNA; 663 BP.
 XX AC AAZ34051;
 XX DT 07-DEC-1999 (first entry)
 XX DE Human PRO772 nucleotide sequence.
 XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein; ss;
 XX OS Homo sapiens.
 XX PN WO946281-A2.
 XX PD 16-SEP-1999.
 XX PF 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 25-MAR-1998; 98US-0078939.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079556.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 15-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081852.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082168.
 PR 22-APR-1998; 98US-0082269.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 23-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 98US-0082796.

	Matches	504; conservative	0;	Mismatches	0;	Indels	159;	Gaps	1;
PR	27-APR-1998:	98US-0083336.							
PR	28-APR-1998:	98US-0083322.							
PR	29-APR-1998:	98US-0083392.							
PR	29-APR-1998:	98US-0083495.							
PR	29-APR-1998:	98US-0083496.							
PR	29-APR-1998:	98US-0083499.							
PR	29-APR-1998:	98US-0083500.							
PR	29-APR-1998:	98US-0083545.							
PR	29-APR-1998:	98US-0083558.							
PR	29-APR-1998:	98US-0083559.							
PR	30-APR-1998:	98US-0083742.							
PR	05-MAY-1998:	98US-0084366.							
PR	06-MAY-1998:	98US-0084414.							
PR	06-MAY-1998:	98US-0084441.							
PR	07-MAY-1998:	98US-0084598.							
PR	07-MAY-1998:	98US-0084600.							
PR	07-MAY-1998:	98US-0084627.							
PR	13-MAY-1998:	98US-008523.							
PR	13-MAY-1998:	98US-0085338.							
PR	13-MAY-1998:	98US-0085339.							
PR	15-MAY-1998:	98US-0085573.							
PR	15-MAY-1998:	98US-0085579.							
PR	15-MAY-1998:	98US-0085580.							
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PR	15-MAY-1998:	98US-0085589.							
PR	15-MAY-1998:	98US-0085597.							
PR	15-MAY-1998:	98US-0085700.							
PR	18-MAY-1998:	98US-0085704.							
PR	22-MAY-1998:	98US-0086192.							
PR	22-MAY-1998:	98US-0086194.							
PR	22-MAY-1998:	98US-0086430.							
PR	28-MAY-1998:	98US-0086486.							
PR	28-MAY-1998:	98US-0087196.							
PR	28-MAY-1998:	98US-0087208.							
PR	30-JUL-1998:	98US-0094551.							
PR	11-SEP-1998:	98US-0100038.							
XX	(GETH) GENENTECH INC.								
PI	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;								
XX	DR								
XX	PPI; 1999-551359/46.								
XX	P-PSDB; AAY41713.								
PT	New secreted and transmembrane polypeptides and their polynucleotides, cancers and cellular adhesion disorders -								
XX	PS	Claim 2; Fig 69; 530pp; English.							
CC	The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ33898, and AAY41685 to AYV41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention.								
SQ	Sequence 663 BP; 180 A; 137 C; 153 G; 193 T; 0 other;								
Query Match	62.7%	Score 335;	DB 20;	Length 663;					
Best Local Similarity	76.0%;	Pred. No. 9.8e-64;							

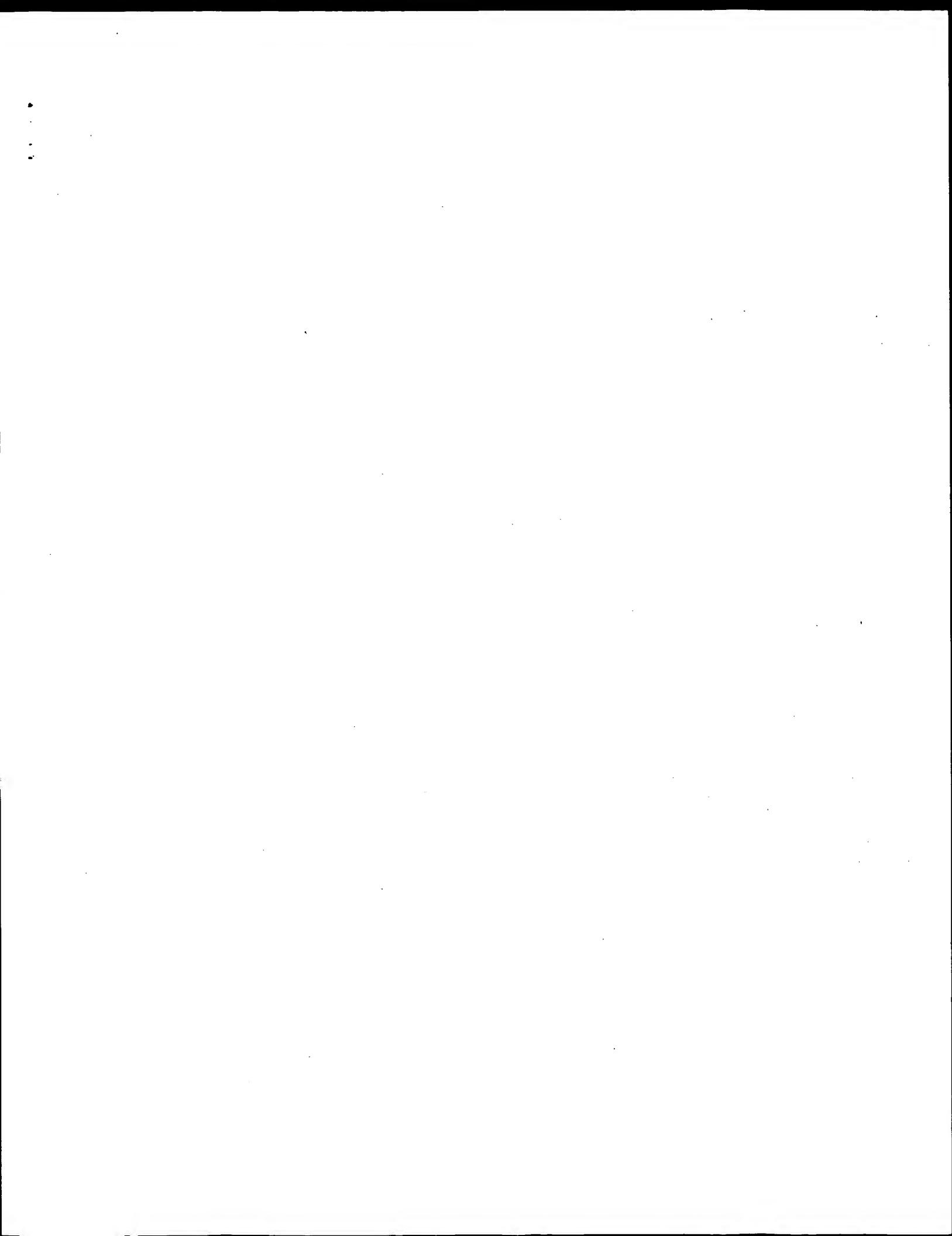
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Job time : 219 secs

The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ33898, and AAY41685 to AYV41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention.

SQ Sequence 663 BP; 180 A; 137 C; 153 G; 193 T; 0 other;

Query Match 62.7%; Score 335; DB 20; Length 663;

Best Local Similarity 76.0%; Pred. No. 9.8e-64;



GnCore version 5.1.6										
Copyright (c) 1993 - 2003 Compugen Ltd.										
OM nucleic - nucleic search, using sw model										
Run on:										
June 25, 2003, 10:08:11 ; Search time 65 Seconds (without alignments)										
2519.468 Million cell updates/sec										
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Gapop:	10.0 , Gapext: 1.0	2	41.2	7.7	3459	2	US-08-980-060-3	32	42	
Searched:	441362 seqs, 153338381 residues	3	33	41.2	7.7	3459	4	US-08-307-185-3	33	42
Total number of hits satisfying chosen parameters:	882724	4	34	41	7.7	218	4	US-09-480-921B-18	34	42
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Maximum DB seq length: 2000000000		6	36	40.8	7.6	1046	1	US-08-484-332C-4	36	42
Post-processing: Minimum Match 0%		7	37	40.6	7.6	731	1	US-08-451-05A-2	37	42
Maximum Match 100%		8	38	40.6	7.6	2444	3	US-08-906-791-1	38	42
Listing first 45 summaries		9	39	40.6	7.6	2625	4	US-08-245-041-18	39	42
Result	Query Length	DB ID	Score	%	No.	40	40.4	7.6	1253	2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
RESULT 1										
Sequence 98, Appl	US-09-149-476-98	1	Patent No. 6420526							
GENERAL INFORMATION:										
APPLICANT: Rosen et al.										
FILE REFERENCE: PZ02021										
TIME OF INVENTION: 186										
CURRENT APPLICATION NUMBER: US/09/149,476										
CURRENT FILING DATE: 1998-09-08										
EARLIER APPLICATION NUMBER: PCT/US98/04493										
EARLIER FILING DATE: 1998-03-06										
EARLIER APPLICATION NUMBER: 60/040,162										
EARLIER FILING DATE: 1997-03-07										
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EARLIER FILING DATE: 1997-03-07	</									

Sequence 193, Appl
Sequence 12, Appl
Sequence 2, Appl
Patent No. 5168051
Sequence 3, Appl
Sequence 3, Appl
Sequence 18, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 18, Appl
Sequence 1, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 10, Appl


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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 91.1%; Score 486.6; DB 4; Length 504;
Best Local Similarity 99.0%; Pred. No. 2,7e-115; Mismatches 0; Indels 1; Gaps 1;
Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 21 CCGAGCTGGGAGAGACAGAGGGAGGGGGCTCCGGGGGTGCGGTTGCTATCGCT 80
Db 1 CGCAGCTGGGAGAGCTGGGGGGG-ACGAGCCGCCGGTGGCTATCGCT 59
Qy 81 TCGGAGAACTACTCAGGGAGCGTGAGAAGAGITGAGGAAGTGTGCTGCTCGGT 140
Db 60 TCGCAGAACCTACTCAGGGAGCGTGAGAAGAGITGAGGAAGTGTGCTGCTCGGT 119
Qy 141 CTGCAGAGCGGAGATGATAACGTCAGTGGCAAGAACATGGCTGGGGCTTCTGCTAGTG 200
Db 120 CTGCAGAGCGGAGATGATAACGTCAGTGGCAAGAACATGGCTGGGGCTTCTGCTAGTG 179
Qy 201 TGAAGGGCACCGAGAGAGTGCTGGGGCTTGGATTATCACTCACTGTGTAACAGAT 260
Db 180 TGAAAGGCACGAGTGAGAAGTGCTGGGGCTTCTGCTAGTG 239
Qy 261 TCATGCTATCGATCTGTGACTGTTGCACTGATACAGAACACAGCTGTGACACAGAT 320
Db 240 TCATGCTATCGATCTGTGACTGTTGCACTGATACAGAACACAGCTGTGACACAGAT 299
Qy 321 GAGGGGTGTTGACTTGTGACAGCAGTATGCTGGGGCCCTATTAC 380
Db 300 GAGGGGTGTTGACTTGTGACAGCAGTATGCTGGGGCCCTATTAC 359
Qy 381 GGAAGCTCTGTCATACTCAGGGCTTACAGAACAAAGCTGTGATGAAAGAAG 440
Db 360 GGAAAGCTCTGTCATACTCAGGGCTTACAGAACAAAGCTGTGATGAAAGAAG 419
Qy 441 AACGTTGTTATTTATTTACTTTTGTGATCAAGTATTACATATTCTGTA 500
Db 420 AACGTTGTTATTTATTTACTTTTGTGATCAAGTATTACATATTCTGTA 479
Qy 501 TTCTCCAAAAAAA 525
Db 480 TTCTCCAAAAAAA 504

RESULT 2
US 09-149-476-252
; Sequence 252, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163

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EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-06-22

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EARLIER APPLICATION NUMBER: 60/056, 877
 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 881
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 909
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 875
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 862
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/057, 650
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/056, 884
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/057, 669
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/049, 610
 EARLIER FILING DATE: 1997-06-13
 EARLIER APPLICATION NUMBER: 60/061, 060
 ; EARLIER FILING DATE: 1997-10-02

Query Match 89.6%; Score 478.6; DB 4; Length 506;
 Best Local Similarity 97.4%; Pred. No. 3e-113; Mismatches 484; Conservative 2; Indels 11; Gaps 0; Gaps 0;

Qy	37	GTAAGGGAGGGCGTGTGTCGCCGCGCGGCGCGCTGCTATGCCTTGCTGCAGAACCTACTCA	96
Db	2	GCAAGATTGGCCAGGAACCCSCCGGGTGGCGTTGCTATGCCTTGCTGCAGAACCTACTCA	61
Qy	97	GGCAGCCAGCTGAGAAGAGTGGAGGAAGTGCTGCTGGTCTGCCAGACGGCGATGGA	156
Db	62	GCCAGCCAGCTGAGAAGAGTGGAGGAAGTGCTGCTGGTCTGCCAGACGGCGATGGA	121
Qy	157	TAAGTGAGCCAAATAAACATCGCCCTCTGCTTCAGTGAGAAAGGCCACGTGAA	216
Db	122	TAACGTGAGCCAAATAAACATCGCCCTCTGCTTCAGTGAGAAAGGCCACGTGAA	181
Qy	217	GATGTTGGCACTGATACCCAGAACCCACACATGACAGTGTGGGGGTTGCACT	276
Db	182	GATGCTGGCGCTGGATATATCACTACTGTTAACACAGTATTGCTACGTTATGCTCATGTTAC	241
Qy	277	TGTTTGCACTGATACCCAGAACCCACACATGACAGTGTGGGGGTTGCACT	336
Db	242	TGTTTGCACTGATACCCAGAACCCACACATGACAGTGTGGGGGTTGCACT	301
Qy	337	TGGACAGCACTGATGCTGCTGCGACGGGCCCCCTATTTACCGGAAGCTCTGCTCAA	396
Db	302	TGGACAGCACTGATGCTGCTGCGACGGGCCCCCTATTTACCGGAAGCTCTGCTCAA	361
Qy	397	TCCAGGGCTCTACAGAAAGCTGATGAGAAAGAGTGTGTTGAA	456
Db	362	TCCAGGGCTCTACAGAAAGCTGATGAGAAAGAGTGTGTTGAA	421
Qy	457	TATCTCTTTAGTTAGTACTAAGGATTAACATTTCTGTTGAA	516
Db	422	TATCTCTTTAGTTAGTACTAAGGATTAACATTTCTGKATTTCCAAAAAAA	481
Qy	517	AAAAAA	533
Db	482	AAAAAA	498

RESULT 3
US-09-385-982-95
Sequence 95, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CDDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385, 982
CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328, 111
EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117, 393
EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098, 639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 95
LENGTH: 392
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc. feature
LOCATION: (1)..(392)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-95

Query Match 50.9%; Score 272; DB 4; Length 392;
Best Local Similarity 95.3%; Pred. No. 1.3e-60;
Matches 297; Conservative 0; Mismatches 12; Indels 2; Gaps 2;
QY 226 GCTGGATATTCACTACAGTAAACAGTATCAGTCATCGTATCTGTTGGC 285
Db 43 GCTTGATATTCACTACAGTAAACAGTATCAGTCATCGTATCTGTTGGC 102
QY 286 ACTGAAACCAGAACACACAATGACAGTGGGAGGGGTGTTGCACTGTGACAGC 345
Db 103 ACTGATACCAGAACACACAATGACAGTGGTGGAGGGGTGTTGCACTGTGACAGC 162
QY 346 AGTATGCTGTGTCGGAGGGGCCATTATCCGAAGCTCTTCATACTCCAGCGG 405
Db 163 AGTATGCTGTGTCGGAGGGGCCATTATCCGAAGCTCTTCATACTCCAGCGG 222
QY 405 TCCTTACGAGAAAACGCTGTCATC-AAAAAGAGAGTTGTTATTATTAATCTT 464
Db 223 TCCTTACGAGAAAACGCTGTCATC-AAAAAGAGAGTTGTTATTATTAATCTT 282
QY 465 TTT-AGTTGACTAAGTAAATATTCTGATCTCCAAAAA 523
Db 283 NTAAAGTTGACTAAGTAAATATTCTGATCTCCAAAAA 342
QY 524 AAAAAGAAAAA 534
Db 343 TNNNTTAAA 353

RESULT 4
US-08-545-196B-10
; Sequence 10, Application US/08545196B
; Patent No. 6080577
; GENERAL INFORMATION:
APPLICANT: MEIKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

RESULT 5
US-08-545-196B-12
; Sequence 12, Application US/08545196B
; Patent No. 6080577
; GENERAL INFORMATION:
APPLICANT: MEIKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545, 196B
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32, 350
REFERENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050

COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PE-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545, 196B
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32, 350
REFERENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1582 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

; US-08-545-196B-12

Query Match

Best Local Similarity

Length

Score

DB

3

Length

1582;

Mismatches

0;

Indels

0;

Gaps

0;

Matches

66;

Conservative

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Mismatches

26;

Indels

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Gaps

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Matches

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Conservative

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Mismatches

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Mismatches

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Indels

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Gaps

0;

Matches

66;

Conservative

0;

Mismatches

26;

TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/450,883
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; SEQ ID NO:16;
; LENGTH: 961
; 5.194596-16

Query Match Similarity 8.4%; Score 45; DB 6; Length 961;
; Best Local Similarity 63.3%; Pred. No. 0.015; 0; Mismatches 40; Indels 0; Gaps 0;
; Matches 69; Conservative 0; Mismatches 0;

Qy 426 TGGATGAAAGAAGCTTGTAATTATTTTACTTGTAGTTAGCTAATCTT 485
; Db 852 TACATTA 911

Qy 486 AACATATTCGATCCTCCAAAAAAAANAAAAAAA 534
; Db 912 TATRAATATATATATCTTAAKAAAARAAA 960

RESULT 9
; patent No. 5219739
; ; APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,
; JOHN C.; MITCHELL, RICHARD L.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING bVEGF120 AND
; ; bVEGF121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
; VASCULAR ENDOTHELIAL CELL GROWTH FACTORS, bVEGF120 AND bVEGF121
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/559,041
; FILING DATE: 27-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 450,883
; FILING DATE: 14-DEC-1989
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; ; SEQ ID NO:16;
; LENGTH: 961
; 5.219739-16

Query Match Similarity 8.4%; Score 45; DB 6; Length 961;
; Best Local Similarity 63.3%; Pred. No. 0.015; 0; Mismatches 40; Indels 0; Gaps 0;
; Matches 69; Conservative 0; Mismatches 0;

Qy 426 TGGATGAAAGAAGCTTGTAATTATTTTACTTGTAGTTAGCTAATCTT 485
; Db 852 TACATTA 911

Qy 486 AACATATTCGATCCTCCAAAAAAAANAAAAAAA 534
; Db 912 TATRAATATATATCTTAAKAAAARAAA 960

RESULT 10
; US-09-276-400-1
; Sequence 1, Application US/09276400
; Patent No. 6140056
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: MNT-073
; CURRENT APPLICATION NUMBER: US/09/276,400
; CURRENT FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0

Query Match Similarity 8.4%; Score 45; DB 6; Length 961;
; Best Local Similarity 63.3%; Pred. No. 0.015; 0; Mismatches 40; Indels 0; Gaps 0;
; Matches 69; Conservative 0; Mismatches 0;

Qy 426 TGGATGAAAGAAGCTTGTAATTATTTTACTTGTAGTTAGCTAATCTT 485
; Db 852 TACATTA 911

Qy 486 AACATATTCGATCCTCCAAAAAAAANAAAAAAA 534
; Db 912 TATRAATATATATCTTAAKAAAARAAA 960

RESULT 11
; US-09-448-075-1
; Sequence 1, Application US/09448076
; Patent No. 6300092
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran et al.
; TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
; FILE REFERENCE: MNT-073CP
; CURRENT APPLICATION NUMBER: US/09/448,076
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/117,580
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 09/276,400
; EARLIER FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (143)..(2401)

Query Match Similarity 8.4%; Score 44.6; DB 4; Length 2920;
; Best Local Similarity 68.1%; Pred. No. 0.03; 29; Indels 0; Gaps 0;
; Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 444 TTTGTTATTTATATCTTTTGTGACTAGTAACTATTTCTGATTC 503
; Db 2820 TTCTACTATATAATGTTGCTAGTATAATTTTTATAAAGTTCTGTGATP 2879

Qy 504 TTCCAAAAAAAANAAAAAAA 534
; Db 2880 CTTCAGAAAAAAAANAAAAAAA 2910

RESULT 12
; US-09-702-572-1
; Sequence 1, Application US/09702572
; Patent No. 6391602
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: MNT-073
; CURRENT APPLICATION NUMBER: US/09/702,572
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25

CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,306
 FILING DATE: 15-APR-1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.422C1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 22:

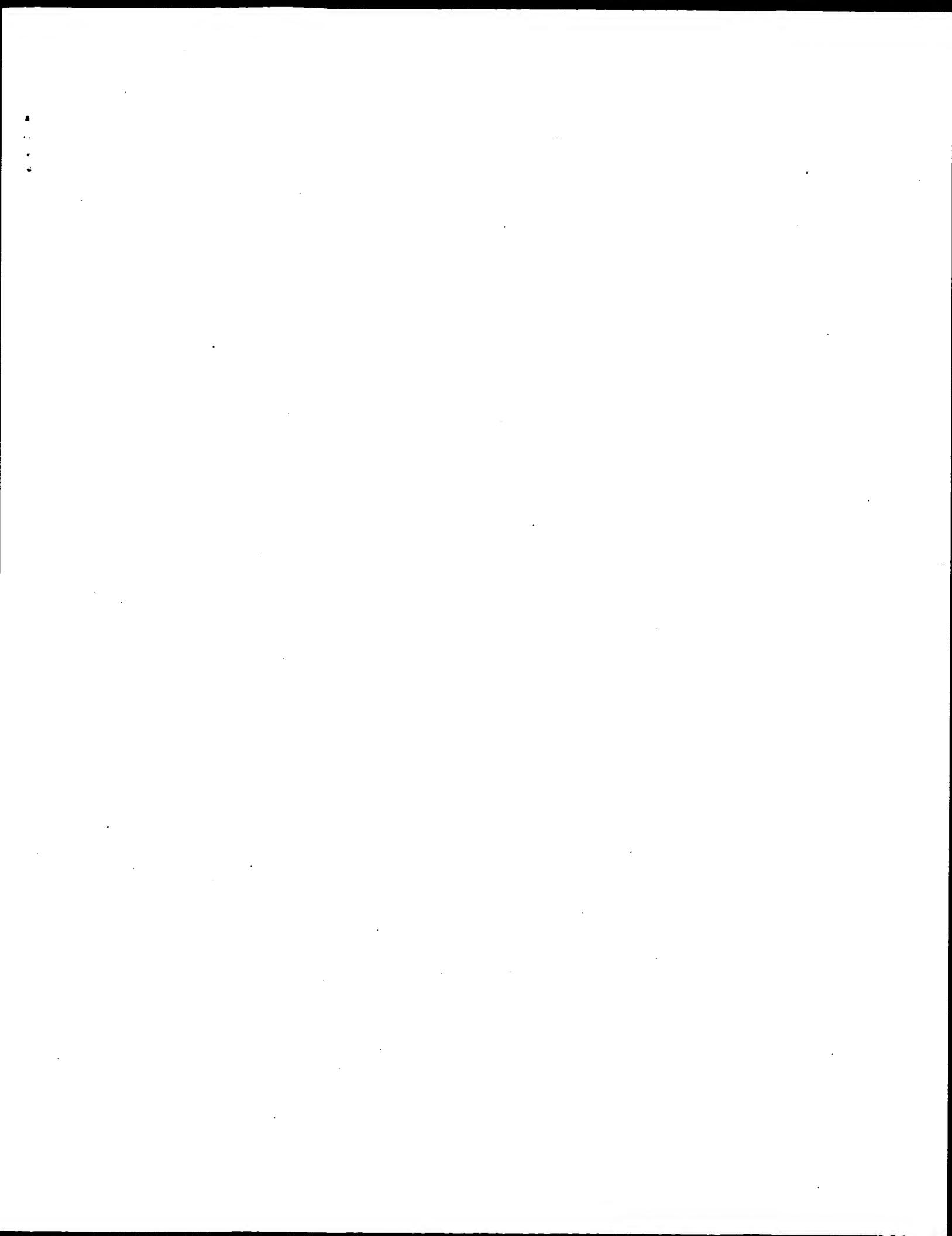
SEQUENCE CHARACTERISTICS:
 LENGTH: 581 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-834-306-22

Query Match 8.3%; Score 44.2; DB 3; Length 581;
 Best Local Similarity 68.5%; Pred. No. 0.02; Matches 61; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY	446	TCTGTAATTTATAATTACTTCTTGTAGTGATCTAAGTAAACATATTCTCTGTTATTCTT	505
Db	484	TCTTTTTATATGCTTTTTTATGAGAGATGCTCTGTTGTTGTTT	543
QY	506	CGAAAAAAAAGAAAAAAAAGAAAAAAA 534	
Db	544	CAAAAAAAAAGAAAAAAAAGAAAAAAA 572	

Search completed: June 25, 2003, 11:55:46
 Job time : 68 secs



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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 11:30:45 ; Search time 139 Seconds
(without alignments)

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

total number of hits satisfying chosen parameters: 2085038

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_5/podata/1/pubpna/us07_PUBCOMB.seq:*
- 2: /cgn2_6/podata/1/pubpna/pcr_NEW_PUB.seq:*
- 3: /cgn2_6/podata/1/pubpna/us06_NEW_PUB.seq:*
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- 5: /cgn2_6/podata/1/pubpna/us07_NEW_PUB.seq:*
- 6: /cgn2_6/podata/1/pubpna/pctus_PUBCOMB.seq:*
- 7: /cgn2_5/podata/1/pubpna/us08_NEW_PUB.seq:*
- 8: /cgn2_6/podata/1/pubpna/us08_PUBCOMB.seq:*
- 9: /cgn2_6/podata/1/pubpna/us09_NEW_PUB.seq:*
- 10: /cgn2_6/podata/1/pubpna/us09_PUBCOMB.seq:*
- 11: /cgn2_6/podata/1/pubpna/us10_NEW_PUB.seq:*
- 12: /cgn2_6/podata/1/pubpna/us10_PUBCOMB.seq:*
- 13: /cgn2_6/podata/1/pubpna/us10_NEW_PUB.seq:*
- 14: /cgn2_6/podata/1/pubpna/us60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score or the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	534	100.0	534 10 US-09-801-115-1	Sequence 1; Appl
2	497.2	93.1	558 9 US-10-106-698-1927	Sequence 1227; Ap
3	486.1	91.1	504 9 US-09-803-391-98	Sequence 98; Ap
4	478.6	89.6	506 9 US-09-803-391-252	Sequence 252; Ap
5	460.2	86.2	512 9 US-09-918-995-19489	Sequence 19489; A
6	425	79.6	4339 9 US-09-822-846-397	Sequence 397; Ap
7	404	75.7	4222 9 US-09-918-6534	Sequence 6534; Ap
8	335	62.7	663 9 US-09-978-295M-189	Sequence 189; App
9	335	62.7	663 9 US-09-978-697-189	Sequence 189; App
10	335	62.7	663 9 US-09-977-192-189	Sequence 189; App
11	335	62.7	663 9 US-09-998-832A-189	Sequence 189; App
12	335	62.7	663 9 US-09-978-189-189	Sequence 189; App
13	335	62.7	663 9 US-09-977-608A-189	Sequence 189; App
14	335	62.7	663 9 US-09-978-191A-189	Sequence 189; App
15	335	62.7	663 9 US-09-978-403A-189	Sequence 189; App
16	335	62.7	663 9 US-09-978-564A-189	Sequence 189; App
17	335	62.7	663 9 US-09-978-585A-189	Sequence 189; App
18	335	62.7	663 9 US-10-017-081A-189	Sequence 189; App
19	335	62.7	663 9 US-09-978-824-189	Sequence 189; App

ALIGNMENTS

RESULT 1

US-09-801-115-1

; Sequence 1, Application US/09801115

; Patent No. US2002000182BA1

; GENERAL INFORMATION:

; APPLICANT: Ma, D.

; APPLICANT: Han, W.

; APPLICANT: Zhang, Y.

; APPLICANT: Song, Q.

; APPLICANT: Li, C.

; APPLICANT: Huang, J.

; APPLICANT: Tang, J.

; APPLICANT: Chen, G.

; TITLE OF INVENTION: CHEMOKINE LIKE FACTOR(CKLF) WITH CHEMOTACTIC AND HEMATOPOIETIC ACTIVITIES

; TITLE OF INVENTION: STIMULATING ACTIVITIES

; FILE REFERENCE: 10776-03-999

; CURRENT APPLICATION NUMBER: US/09-801-115

; CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: PCT/CN00/00026

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 99107284.7

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 1

LENGTH: 534

TYPE: DNA

ORGANISM: Homo sapiens

US-09-801-115-1

Query Match Best Local Similarity 100.0%; Score 534; DB 10; Length 534; Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAATCTGAGTGAGCTGAGCCGAGCTGGCGAGAGTAGGGAGGGGCGCTCGCGCG 60

Db 1 GTGCCAATCTGAGTGAGCTGAGCCGAGCTGGCGAGAGTAGGGAGGGGCGCTCGCGCG 60

QY 61 CGGTGGCGTGTGTTACGCCTCCGAGAACCTACTCAGGCAGCCGCTGGCGGGCTCCGCCG 120

Db 61 CGGTGGCGTGTGTTACGCCTCCGAGAACCTACTCAGGCAGCCGCTGGCGGGCTCCGCCG 120

QY 121 GGAAAGTGTGCGTGTGGTCAGACGGCGATGAGATACGGTCAGCCGAATAAACCA 180

RESULT 4
US-09-809-391-252
Sequence 252, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-755
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19489
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(512)
; OTHER INFORMATION: n = A,T,C or G
; US-09-809-391-252
Query Match 89.6%; Score 478.6; DB 9; Length 506;
Best Local Similarity 97.4%; Pred. No. 1e-110; Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
Matches 484;
Qy 37 GTAGGGAGGGGGTGCCTCCGCGCGGGGTGCTATCGCTCGCAGAACCTACTA 96
Db 2 GCAGGATTGGCCAGACCCSCCGCGGTGCGGGTTCTATCGCTCGCAGAACCTACTA 61
Qy 97 GGAGGCCAGCTGAGAAGAGTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGATGGA 156
Db 62 GCGAGGCCAGCTGAGAAGAGTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGATGGA 121
Qy 157 TAACTGTCAGCCGAAATAAACATGCCCTCTCTCTAGTGCAAGGCCAGTGAA 216
Db 122 TAACGTGAGGCCAAATAAACATGCCCTCTCTAGTGCAAGGCCAGTGAA 181
Qy 217 GATGCTGCGGCCTGCGATATTATCAACTCACTGCTACAGAACACTATTCATGCTCATCGTAC 276
Db 182 GATGCTGCGGCCTGCGATATTATCAACTCACTGCTACAGAACACTATTCATGCTCATCGTAC 241
Qy 277 TGTGTCGCACTGATACCGAACACACATGACAGTGTGGGGGTGTTGCACT 336
Db 242 TGTGTCGCACTGATACCGAACACACATGACAGTGTGGGGGTGTTGCACT 301
Qy 337 TGTGACAGCAGTACGCTGCTGCGAGGGGCCCTATTAACGGAAAGCTCTGCTCATCCAGGGCTCTACCGA 416
Db 302 TGTGACAGCAGTACGCTGCTGCGAGGGGCCCTATTAACGGAAAGCTCTGCTCATCCAGGGCTCTACCGA 361
Qy 397 TOCCAGGGTCCATTACCGAACACACATGACAGTGTGGGGGTGTTGCACT 456
Db 362 TCCAGGGTCCATTACCGAACACACATGACAGTGTGGGGGTGTTGCACT 421
Qy 457 TATTAATTAGTTAGTGTACGATTAACATATTCTGATTCCTCCAAAAAAA 516
Db 422 TATTAATTAGTTAGTGTACGATTAACATATTCTGATTCCTCCAAAAAAA 481
Qy 517 AAAAAMAAAAMAAA 533
Db 482 AAAAAMAAAAMAAA 498
RESULT 5
US-09-918-995-19489

; Sequence 19489, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-755
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19489
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(512)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-19489
Query Match 86.2%; Score 460.2; DB 9; Length 512;
Best Local Similarity 99.1%; Pred. No. 4.3e-106;
Matches 462; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 57 GCGCGGGGGGGGGGTGATGCGCTGCGAGACACTACGCGAGCGAGCTGAGAACAGT 116
Db 47 GCGGGGGGGGGGGGTGATGCGCTGCGAGACACTACGCGAGCGAGCTGAGAACAGT 106
Qy 117 TGAGGGAAGTGCCTGCTGCTGGGTCTGCAGACGAGAACAGT 176
Db 107 TGAGGGAAGTGCCTGCTGCTGGGTCTGCAGACGAGAACAGT 166
Qy 177 AACATCGCCCTCTGCTCAGTGAAAGGCCAGGAGGAGATGCTGGGTGAGATTA 236
Db 167 AACATCGCCCTCTGCTCAGTGAAAGGCCAGGAGGAGATGCTGGGTGAGATTA 226
Qy 237 TCAACTCACHTGCTACACAGTATTCATGCTCATGTTCTGTTGCACTGACAG 296
Db 227 TCAACTCACHTGCTACACAGTATTCATGCTCATGTTCTGTTGCACTGACAG 286
Qy 297 AAACCCACAATGTCAGTGTGGAGGGGTGTTGACTTGAGACACAGATGCTC 356
Db 287 AAACCCACAATGTCAGTGTGGAGGGGTGTTGACTTGAGACACAGATGCTC 346
Qy 357 TTGGCAGGGCCCTTATTAACGGAACTCTCTGCTCATCCAGGGCTCTACCGA 416
Db 347 TTGGCAGGGCCCTTATTAACGGAACTCTCTGCTCATCCAGGGCTCTACCGA 406
Qy 417 AAACGCTGCACTAAAGAAGAGTTGTGAAATTATACCTTTAGTTGATA 476
Db 407 AAACGCTGCACTAAAGAAGAGTTGTGAAATTATACCTTTAGTTGATA 466
Qy 477 CTAACTTAAACATATTCTGATTCCTCCAAAAAAA 522
Db 467 CTAACTTAAACATATTCTGATTCCTCCAAAAAAA 512
RESULT 6
US-09-822-846-397
; Sequence 397, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.

APPLICANT: Steiniger II, Robert J.
 APPLICANT: Bowman, Michael R.
 APPLICANT: Spaulding, Vikki
 APPLICANT: Wong, Gordon G.
 APPLICANT: Clark, Hilary
 APPLICANT: Fechter, Kim
 APPLICANT: Hoves, Steven H.
 APPLICANT: Resnick, Richard J.
 APPLICANT: Gulukota, Kamalakar
 APPLICANT: Graham, James R.
 APPLICANT: Genetics Institute, Inc.
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
 FILE REFERENCE: GIN 6400
 CURRENT APPLICATION NUMBER: US/09/822, 846
 PRIORITY FILING DATE: 2001-03-29
 PRIORITY FILING NUMBER: 60/195, 605
 PRIOR FILING DATE: 2000-04-06
 NUMBER OF SEQ ID NOS: 629
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 397
 LENGTH: 439
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-822-846-397

Query Match 79.68; Score 425; DB 9; length 439;
 Best Local Similarity 99.8%; Pred. No. 2.8e-97; Mismatches 0; Indels 0; Gaps 0;
 Matches 436; Conservative 0; MisMatches 0; Indels 1; gaps 1;

QY 72 GCTATCGCTTCAGAACACTACAGCGGAGCAGTGAAGAAGAGTTGGGAAAGTGCTG 131
 1 GGTATGCCCTCCAGAACACTACAGCGGAGCAGTGAAGAAGAGTTGGGAAAGTGCTG 60

QY 132 CNGCTGGCTCAGACGGGATGATACGTCAGCGGAGAATAAACATCGCCCTCT 191
 61 CGCTGGCTCAGACGGGATGATACGTCAGCGGAGAATAAACATCGCCCTCT 120

Db 242 TCACGGTAACAAGTAACTCATGCTCATGTTGTTGCACTGATACAGAACC 301
 121 TCACGGTAACAAGTAACTCATGCTCATGTTGTTGCACTGATACAGAACC 180

Db 302 ACACATTGACAGCTGGAGGGGTGTTGACTGTGACACCAATGCTTGCC 361
 181 ACACATTGACAGCTGGAGGGGTGTTGACTGTGACACCAATGCTTGCC 240

QY 362 GACGGGCCATTATTCAGGAACCTCTGTCATCCAGGGCTTACCGAAGAAG 421
 121 GACGGGCCATTATTCAGGAACCTCTGTCATCCAGGGCTTACCGAAGAAG 300

Db 241 GACGGGCCATTATTCAGGAACCTCTGTCATCCAGGGCTTACCGAAGAAG 300

QY 422 CCTGTGCATGAAAAAAGAGTTGTTGTTATTTATTTACTTTTGTAGTAAAG 481
 120 CCTGTGCATGAAAAAAGAGTTGTTGTTATTTATTTACTTTTGTAGTAAAG 360

Db 301 CCTGGCAGGAAAAAAGAGTTGTTGTTATTTATTTACTTTTGTAGTAAAG 360

QY 482 TATPAAACATATTCTGTATTCCTCCAAAAAAAAGAAAAAAA 525
 180 TATPAAACATATTCTGTATTCCTCCAAAAAAAAGAAAAAAA 404

Db 361 TATPAAACATATTCTGTATTCCTCCAAAAAAAAGAAAAAAA 404

RESULT 8
 US-09-822-846-397
 Sequence 189, Application US/09/78295A
 ; patent No. US200215006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Geritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Paul Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillman, Kenneth J.
 ; APPLICANT: Kijain, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel

RESULT 7
 US-09-918-995-6534
 Sequence 6534, Application US/09/18995
 ; Publication No. US2003073623A1

GENERAL INFORMATION:
 ; APPLICANT: Byseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS cDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918, 995
 ; CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235, 076
 PRIORITY FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 6234
 LENGTH: 422
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-918-995-6534

Query Match 75.7%; Score 404; DB 9; Length 422;
 Best Local Similarity 100.0%; Pred. No. 5.3e-92; Mismatches 0; Indels 0; Gaps 0;
 Matches 404; Conservative 0; MisMatches 0; Indels 0; gaps 0;

QY 122 GAATGGCTCTGCTGAGTAACGTGAGCCACGTGAGAGATGCTGGGCTGGATATTCAC 181
 1 GAATGGCTCTGCTGAGTAACGTGAGCCACGTGAGAGATGCTGGGCTGGATATTCAC 60

Db 182 CGCCCTTCGCTGAGTAACGTGAGCCACGTGAGAGATGCTGGGCTGGATATTCAC 241
 61 CGCCCTTCGCTGAGTAACGTGAGCCACGTGAGAGATGCTGGGCTGGATATTCAC 120

QY 242 TCACGGTAACAAGTAACTCATGCTCATGTTGTTGCACTGATACAGAACC 301
 121 TCACGGTAACAAGTAACTCATGCTCATGTTGTTGCACTGATACAGAACC 180

Db 302 ACACATTGACAGCTGGAGGGGTGTTGACTGTGACACCAATGCTTGCC 361
 181 ACACATTGACAGCTGGAGGGGTGTTGACTGTGACACCAATGCTTGCC 240

QY 362 GACGGGCCATTATTCAGGAACCTCTGTCATCCAGGGCTTACCGAAGAAG 421
 121 GACGGGCCATTATTCAGGAACCTCTGTCATCCAGGGCTTACCGAAGAAG 300

Db 241 GACGGGCCATTATTCAGGAACCTCTGTCATCCAGGGCTTACCGAAGAAG 300

QY 422 CCTGTGCATGAAAAAAGAGTTGTTGTTATTTATTTACTTTTGTAGTAAAG 481
 120 CCTGTGCATGAAAAAAGAGTTGTTGTTATTTATTTACTTTTGTAGTAAAG 360

Db 301 CCTGGCAGGAAAAAAGAGTTGTTGTTATTTATTTACTTTTGTAGTAAAG 360

QY 482 TATPAAACATATTCTGTATTCCTCCAAAAAAAAGAAAAAAA 525
 180 TATPAAACATATTCTGTATTCCTCCAAAAAAAAGAAAAAAA 404

Db 361 TATPAAACATATTCTGTATTCCTCCAAAAAAAAGAAAAAAA 404

APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William T
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C11
 CURRENT APPLICATION NUMBER: US/09/978, 295A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918855
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/066250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/055311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/056364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/07450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/078004
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/078885
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079565
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079924
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080170
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082568
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/083392
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 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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 TITLE OF INVENTION: Acids Encoding the Same
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 US-09-978,192A-189
 Sequence 189, Application US/09/978,192A
 GENERAL INFORMATION:
 Patent No. US200217753A1
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kjavian, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paon, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shefton, David L.
 APPLICANT: Stewart, Timothy A.

PRIOR FILING DATE: 1998-04-08
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PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;
Best Local Similarity 76.0%; Pred. No. 1.6e-74; Mismatches 0; Indels 159; Gaps 1;
Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

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RESULT 11

US-09-999-832A-189
Sequence 189, Application US/09999832A
Publication No. US2002019270611

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2630PIC3

CURRENT APPLICATION NUMBER: US/09/999, 832A

CURRENT FILING DATE: 2001-10-24

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PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match Best local similarity 76.7%; Score 335; DB 9; Length 663;
Matches 504; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

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Db 61 CGCAGAACCTACTCGGGACCCACCTGAGAGTGTAGGGAAAGTGCTGCCTGCTGGTC 120
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RESULT 12 US-09-978-189-189
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; Publication No. US2003004102A1
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; APPLICANT: Asikenazi, Avi
; APPLICANT: Baker, Kevin P
; APPLICANT: Bottstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eatto, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
 FILE REFERENCE: P230PIC7
 CURRENT APPLICATION NUMBER: US/09/978, 189
 CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;
Best Local Similarity 76.0%; Pred. No. 1.6e-74; 0; Mismatches 504; Conservative 0; Indels 159; Gaps 1; Matches 504;

QY 463 TTTTGTGTTGATACTAAGTATAACATATTCTGTATTCCTCCAAAAAAANAAA 522
Db 601 TTTCAGTTGATACATACTTAAACATATTCTGTATTCCTCCAAAAAAANAAA 660
OY 523 AAA 525
Db 661 AAA 663

RESULT 13
US-09-978-608A-189
Sequence 189, Application US/09978608A
Publication No. US20030045462A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bottstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Klaevin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Paln
; SEO ID NO 189
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-978-608A-189

Query Match 62.7%; Score 335; DB 9; Length 663;
Best Local Similarity 76.0%; Pred. No. 1.6e-74; 0; Mismatches 504; Conservative 0; Indels 159; Gaps 1; Matches 504;

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Db 1 CGAGCTGGGAGAGTAGGGGAGGGGGCTCTCCCGGTCGGGTGCTATCGTT 60
OY 22 CGAGCTGGGAGAGTAGGGGAGGGGGCTCTCCCGGTCGGGTGCTATCGTT 81
Db 82 CGCAGAACCTRACTCGAGCAGCACTGGAGAGAGTGAGGAAGTGCCTGCTCGCTGGTC 141
Db 61 CGCAGAACCTRACTCGAGCAGCACTGGAGAGAGTGAGGAAGTGCCTGCTCGCTGGTC 120
QY 142 TGCAGACGCGATGGTGCCTGCTGGAGAGAGTGAGGAAGTGCCTGCTCGCTGGTC 201
Db 121 TGCAGACGCGATGGTGCCTGCTGGAGAGAGTGAGGAAGTGCCTGCTCGCTGGTC 180
QY 202 GAAGGGCACGCGAGAGTGCTGGGCGACTAACGTGACATCTATGACCTTTAT 229
Db 181 GAAGGGCACGCGAGAGTGCTGGGCGACTAACGTGACATCTATGACCTTTAT 240
QY 230 -----
Db 241 CATCGACAAAGCCCTGACCATATATGTTACACTGGATTTGAAGTACCGTTACTT 300
QY 230 -----
Db 301 ATTTTCATCACTTTATGTACTCAGACTGATCGATAATGAAGTGGTATTGGCC 360
QY 230 -----
Db 361 TTGGCTCTATATATCATCACTCTGGAGGGGGCTTATTACCGGAAGTCTGTGTT 420
QY 283 GGCACTGATACCGAACACACATGACAGTGGGAGGGGTGTTGACTGTGAC 342
Db 421 GGCACTGATACCGAACACACATGACAGTGGGAGGGGTGTTGACTGTGAC 480
QY 343 AGCACTGATACCGAACACACATGACAGTGGGAGGGGTGTTGACTGTGAC 402
Db 481 AGGAGTATGCTGCTGCTGGCAGGGGCCCTTATTACGGAGCTGTGTCATCCAG 540
QY 493 CGCTCTTACCGAACAGGCCCTGTCATGAAAAAAAGAGTTGTTGATTTATATC 462
Db 541 CGGCCCCAACAGAACGCCCTGTCAGAACAAAGAGTTGTTGATTTATATC 600
QY 202 GAAGGCCACCTGAGATGCTGGCCT 229
Db 181 GAAAGCCACCTGAGATGCTGGCCT 240

PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/081229

QY 230 ----- -- 229
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 QY 230 ----- -- 229
 Db 301 ATTTTCATACCTTATATGACTCAGACTGATCGATTATGAACTGTTACCGTATCT 360
 QY 230 ----- -GATATATCACTACTGGAAACACAGTTACATGCTCATGATCTGTT 282
 Db 351 TTTGCTTATATPATCACTACTGGAAACACAGTTACATGCTATGCTATCGPATCAGTT 420
 QY 283 GGCACTGATACCGAACCACACATGACAGTGAGGTGGGGGTGTTGACTGAGC 342
 Db 421 GGCAGTCGTTGCGAGGGGCCCTATTACGGAGGTCTGTGCAATCCAG 480
 QY 343 AGCAGTAGCTGTTGCGAGGGGCCCTATTACGGAGGTCTGTGCAATCCAG 402
 Db 481 AGCAGTAGCTGTTGCGAGGGGCCCTATTACGGAGGTCTGTGCAATCCAG 540
 QY 403 CGCTCCTTACCGAAAAGCCGTGCTGAGAAAAAAGAGGTTGTAATTATAC 462
 Db 541 CGGCTCTTACCAAAAAGCCGTGCAAGAAGAATTGTTGATATAC 600
 QY 523 AAA 525
 Db 661 AAA 663

RESULT 14
 US-09-978-191A-189
 Sequence 189, Application US/09978191A
 GENERAL INFORMATION:
 APPLICANT: Askinenzi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: KJavlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630PIC4
 CURRENT APPLICATION NUMBER: US/09/978,191A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30

Sequence 159, Application US/9978403A
 Publication No. US20030050240A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Boiststein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J
 APPLICANT: Kijaviv, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas P.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: 203301C17
 CURRENT APPLICATION NUMBER: US/09/978,403A
 CURRENT FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
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 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499

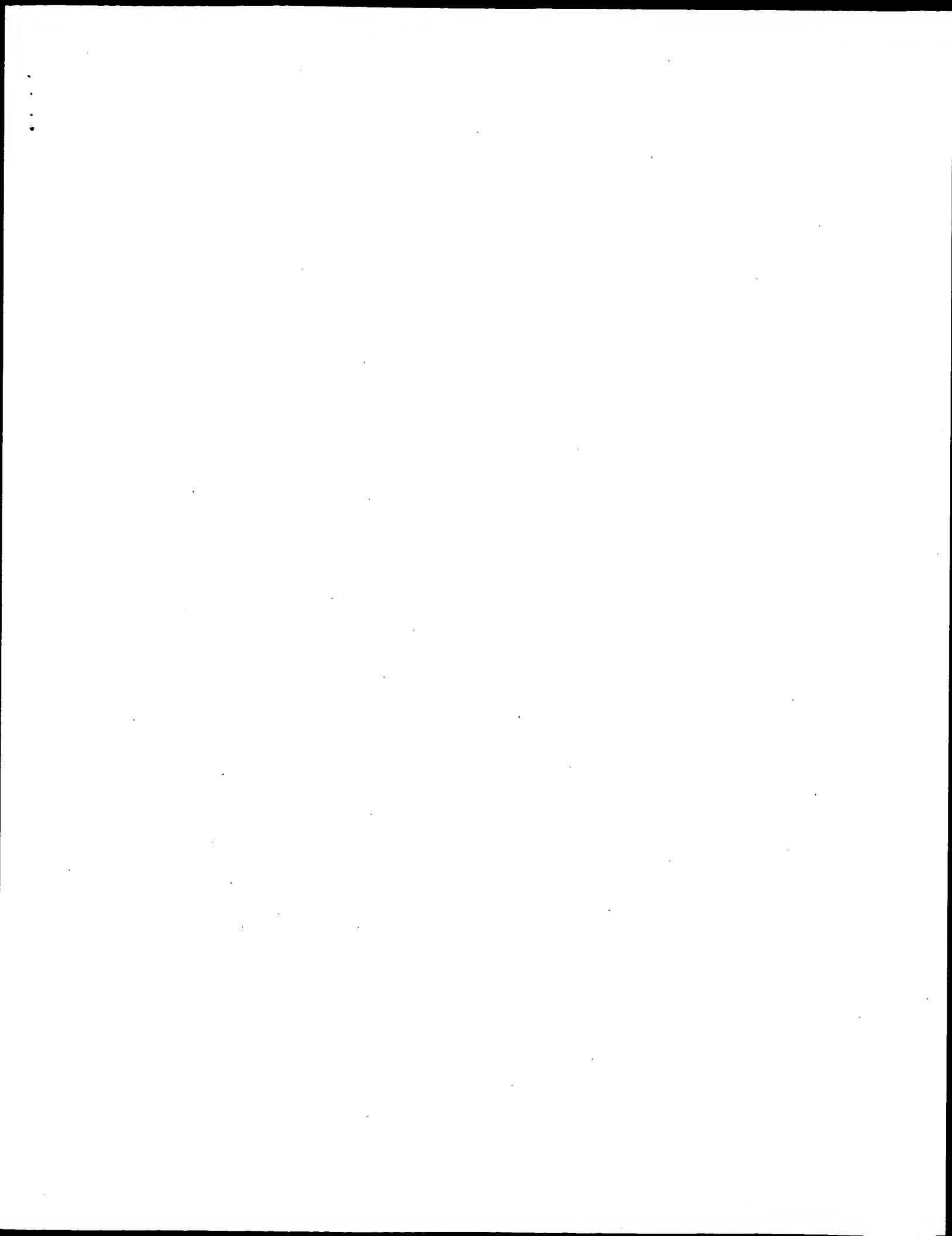
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PRIOR FILING DATE: 1999-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;
Best Local Similarity 76.0%; Pred. No. 1.6e-74; Indels 159; Gaps 1;
Matches 504; Conservative 0; Mismatches 0;

QY 22 CGAGCTGGGAGAAGTAGGGAGGGGGGTGTCGGCCACGGTGTGTT 81
Db 1 CGACGTGGCAGAGTATGGGAGGGCGTGTGCGCGGCGTGTGTT 60
QY 82 CGCAGAACCTACTCAGGCAGCCAGCTGAGAGAGTGAGGAAGTGTGCTGCTGGTC 141
Db 61 CGCAGAACCTACTCAGGCAGCCAGCTGAGAGAGTGAGGAAGTGTGCTGCTGGTC 120
QY 142 TGCAGACGCCATGGATACTGTGACGCCAAATACATGCCCTCTGCTCACTGT 201
Db 121 TGCAGACGCCATGGATACTGTGACGCCAAATACATGCCCTCTGCTCACTGT 180
QY 202 GAAAGCCACGTGAGATGCTGGCTG----- 229

Db 181 GAAAGCCACGTGAGATGCTGCCCTGGCACTACTGTGACATCTATGACCTTTAT 240
Qy 230 ----- 229
Db 241 CATGCCACAGCCCCGTAACCATATATTGTATCTACTGGATTGAGTCAGGTTATCTT 300
Qy 230 -----
Db 301 ATTTCATACCTTTATGACTGAGCTGTGATGATGTTAATGAGTGGTTATTTGGCC 360
Qy 230 -----GATAATCAACTCAGTGTAAACACAGTATCATGCCTCATGTTATCTGTT 282
Db 361 TTGCTGTGATATTAACTACTGCTGTAACACAGTATCATGCCTCATGTTATCTGTT 420
Qy 283 GGCACGTGATACCGAACACACTGTGACGTGTTGAGGGGCTGTGACTGTGAC 342
Db 481 AGCAGTATGCGTGTCTGGCCACACATGTGAGCTGTTGGAGGGGTTGAC 480
Qy 421 GGCACGTGATACCGAACACACTGTGACGTGTTGGAGGGGTTGAC 480
Db 343 ACCGATATGCTGCTGCCGACGGGCCCATTATCCGGAAGTTCTGTTCAATCCAG 402
Qy 463 TTTTACTTGTACTAATGATAAACATATTCTGTTCAAAAAAAA 522
Db 601 TTTTACTTGTACTAATGATAAACATATTCTGTTCAAAAAAAA 660
Qy 523 AAA 525
Db 661 AAA 663

Search completed: June 25, 2003, 12:47:19
Job time : 143 secs



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Gapop 10.0 , Gapext 1.0
Searched: 16154056 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rnd:*

ALIGNMENTS

RESULT 1
BG705303 LOCUS BG705303 DEFINITION 524 bp mRNA LINEAR EST 07-MAY-2001
mRNA sequence.

ACCESSION BG705303
VERSION BG705303.1
KEYWORDS EST,
SOURCE human,
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 524)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
TITLE National Institutes of Health, Mammalian Gene Collection (MGCC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert S. Strausberg, Ph.D.
Email: cgbps-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:
http://image.lnl.gov
Plate: LILN010725 row: 0 column: 01
High quality sequence step: 521.
Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	505.8	94.7	524	BG705303
2	492.4	92.2	962	12 BG249994
3	491.8	92.1	510	12 BF399486
4	487	91.2	781	12 BG229072
5	485.4	90.9	487	13 BM472086
6	482.4	90.3	534	12 BG031757

	AUTHORS	TITLE	NIH-MGC http://mgc.nci.nih.gov/
COMMENT	CDNA Library Preparation: Life Technologies, Inc.	JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
/organism="Homo sapiens"	Unpublished (1999)		
/db_xref="taxon:9606"	Contact: Robert Strausberg, Ph.D.		
/clone_id="NIM_MGC_95"	Email: cgbpls-f@mail.nih.gov		
/tissue_type="hippocampus"	Tissue Procurement: ATCC		
/lab_host="DH10B"	CDNA Library Preparation: Life Technologies, Inc.		
/note="Organ: brain; Vector: pBluescriptR (modified	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI (gtcgag	DNA Sequencing by: Invitae Genomics, Inc.		
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',	Clone distribution: MGC clone distribution information can be		
size-selected for average insert size 2.5 kb and	found through the T.M.A.G.E. Consortium/LLNL at:		
normalized to ROT 5. This is a primary library enriched	http://image.llnl.gov		
for full-length clones and constructed using the	Plate: LLNL0288 row: k column: 15		
Cap-trapper method (Carninci, in preparation). Library	High quality sequence stop: 516.		
constructed by M. Brownstein (NIMH/NICRI, National	Location/Qualifiers		
Institutes of Health). Note: this is a NIH-MGC Library."			
IN			
COUNT			
142 a 113 c 138 g 131 t			
Query Match	94.7%; Score 505 8; DB 12; Length 524;		
St. Local Similarity	99.6%; Pred. No. 8.3e-66;		
Matches	507; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
15 GTGAAACCGAGCTGGCGAGAGTAGGGGGGGCGGTGTCGCCGGGGTGCAGCTGGCT 74			
4 GGGAGCCGAGCTGSGCGAGAGTAGGGGGGGCGGTGTCGCCGGGGTGCAGCTGGCT 63			
75 ATCGCTTCGAGAACCTACTCGAGGAGGAGTAGGGGGGGCGGTGTCGCCGGGGTGCAGCTGGCT 134			
64 ATCGCTTCGAGAACCTACTCGAGGAGGAGTAGGGGGGGCGGTGTCGCCGGGGTGCAGCTGGCT 123			
135 CTGGGCTCGAGACCGATGATAACGTGCAAGCGAAATAAACATGCCCTCTGCT 194			
124 CTGGGCTCGAGACCGATGATAACGTGCAAGCGAAATAAACATGCCCTCTGCT 183			
195 TCAGTGTGAAGGGCCACGTGAGAGAGGTGCGCGGTGATATTACAACCTACTGTACAA 254			
184 TCAGTGTGAAGGGCCACGTGAGAGAGGTGCGCGGTGATATTACAACCTACTGTACAA 243			
255 CAGTACTCATGCTCATGCTCTGTTGTTGCTGAGTACCGAGAACACACATGAG 314			
244 CAGTACTCATGCTCATGCTCTGTTGCTGAGTACCGAGAACACACATGAG 303			
315 TTGGTGGAGGGGTGTTGCACTTGACAGCGATGCTGCTGTCGCCGAGGGCCCTA 374			
304 TTGGTGGAGGGGTGTTGCACTTGACAGCGATGCTGCTGTCGCCGAGGGCCCTA 363			
375 TTACCGGAAGCTCTGTCATGCCAGGGTCTTACCCAGAAAAGSCTGTGTCATGAA 434			
364 TTACCGGAAGCTCTGTCATGCCAGGGTCTTACCCAGAAAAGGCTGTGTCATGAA 423			
435 AAAAGAAGTTGTAATTATATACCTTTGTTGATTAAGTTAACATTT 494			
424 AAAAGAAGTTGTAATTATACCTTTGTTGATTAAGTTAACATTT 483			
495 TCTGTTTCTCCAAAAAAAGAAAA 523			
484 TCTGTTTCTCCAAAAAAAGAAAA 512			
IN			
COUNT			
334 a 199 c 288 g 141 t			
FEATURES	source		
ORIGIN			
BASE COUNT			
Query Match	92.2%; Score 492.4; DB 12; Length 962;		
St. Local Similarity	99.6%; Pred. No. 5e-64;		
Matches	504; Conservative 0; Mismatches 1; Indels 1; Gaps 1;		
QY			
DO	1 GCGGAGAGTAGGGAGGGCGGTGTCGCCGGGGTGGCGTTATGCTTCAGAA 88		
QY	89 CCTACTGGGAGCCACGTGAGAGAGTGTGAGGAAGTGTGCTGCTGGCTGAGAC 148		
DO	61 CCTACTGGGAGCCACGTGAGAGAGTGTGCTGCTGGCTGAGAC 120		
QY	149 GCGATGAGTAAGTGCAAGCCAAATAAACATGCCCTGTGTCAGTAAAGC 208		
DO	121 GGATGTGTAAGTGTGAGGCCAAATAAACATGCCCTGTGTCAGTAAAGC 180		
QY	209 CACGTGAGATGCTGGGGCTGATATACTACACTGCTGTCAGTAAACACATATCATGCC 266		
DO	181 CACGTGAGATGCTGGGGCTGATATACTACACTGCTGTCAGTAAACACATATCATGCC 240		
QY	269 ATCGTATCTGTTGTCATGATACCGAACACACACATGACGCTGCTGTTGGGGGT 328		
DO	241 ATCGTATCTGTTGTCATGATACCGAACACACACATGACGCTGCTGTTGGGGGT 300		
QY	329 TTGCACTTGACAGCGAGAGCTCTTCCGGGGGCCATTACCGAAGCT 388		
DO	301 TTGCACTTGACAGCGAGAGCTCTTCCGGGGGCCATTACCGAAGCT 360		
QY	389 CIGTCAATCCCGCGGTCCATTACCGAAGAAAGCGCTGTCATGAAAGAGTTG 448		
DB	361 CIGTCAATCCCGCGGTCCATTACCGAAGAAAGCGCTGTCATGAAAGAG-TTG 419		
QY	449 TAATTATATACCTTTGTTGATTAAGTTAACATTTCTGTTCTCCA 508		
DB	420 TAATTATATACCTTTGTTGATTAAGTTAACATTTCTGTTCTCCA 479		
QY	509 AAAAAGAAAAAAAGAAAA 534		
DB	480 CAAAGAAAAAAAGAAAA 505		
RESULT 3			
PR300095 /C			
GENE			
PROTEIN			
PROTEIN DOMAIN			
HOMOLOGUE			
FUNCTION			
STRUCTURE			
ORGANISM			
MAMMALIA			
BUTHERIA			
PRIMATES			
CATARRHINI			
HOMINIDAE			
HOMO			
SAPIENS			
HUMAN			
EUKARYOTA			
METAZOA			
CHORDATA			
CRANIATA			
VERTEBRATA			
BUTEOESTOMI			
1 (bases 1 to 962)			

LOCUS	BFF99486	510 bp	mRNA	linear	EST 27-Nov-2000	QY	268	CATGGTATCTGTTGCACTGATACCAGAACACACATGACAGTGCGGAGGGT	327
DEFINITION	UI-R-CAI-bjb-b-12-0-UI..sl	UI-R-CAI	Rattus norvegicus	cDNA clone					
UI-R-CAI-bjb-b-12-0-UI	3'	mRNA sequence.							
ACCESSION	BFF99486								
VERSION	BFF99486.1								
KEYWORDS	EST;								
SOURCE	Norway rat.								
ORGANISM	Rattus norvegicus								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;									
REFERENCE									
AUTHORS	Ronaldo,M.F., Lennon,G. and Soares,M.B.								
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery								
JOURNAL	Genome Res. 6 (9), 791-806 (1996)								
MEDLINE	9704477								
COMMENT	Program for Rat Gene Discovery and Mapping								
POLY=A	Yes								
FEATURES	Location/Qualifiers								
source	I .. .510								
/organism="Rattus norvegicus"									
/strain="Sprague-Dawley"									
/db_xref="taxon:10116"									
/clone="UI-R-CAI-bjb-b-12-0-UI"									
/clone_id="UI-R-CAI"									
/lab_host="DHIOB (Life Technologies)"									
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAI library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla,pons , midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratech.eng.uiowa.edu . The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)									
BASE COUNT	a 130 a	c 131 c	t 104 g	t 145 t					
ORIGIN									
Query Match	92.1%	Score 491.8;	DB 12;	Length 510;					
Best Local Similarity	99.6%	Pred. No. 9.9e-64;	Matches 493;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
QY	28	GGGGAGAGTAGGGAGGCGCGTCGCCTCGCGCGGTGCTATCGCTCGAGA	87						
Db	495	GGCGAGAGTAGGGAGGCGCGTCGCCTCGCGCGGTGCTATCGCTCGAGA	436						
QY	88	ACCTACTGGAGCCACTGAGAAGTGTAGCGGAAGTGTCTGCTGCTGAGA	147						
Db	435	ACCTACTGGAGCCACTGAGAAGTGTAGCGGAAGTGTCTGCTGCTGAGA	376						
QY	148	CGCGATGATAAAGTCGCCGAAATAACATGCCCTCTGCTCAGTGAAAGG	207						
Db	375	CGCGATGATAAAGTCGCCGAAATAACATGCCCTCTGCTCAGTGAAAGG	316						
QY	208	CCACGTGAGATGCTGCCGCTGATATCACTCACTGGACACAGATTATCATG	267						
Db	315	CCACGTGAGATGCTGCCGCTGATATCACTCACTGGACACAGATTATCATG	256						
BASE COUNT	a 228 a	c 157 c	t 233 g	t 163 t					
ORIGIN									
Query Match	91.2%	score 487;	DB 12;	Length 781;					
Best Local Similarity	98.7%	Pred. No. 3.7e-63;							

	found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov
Plate:	LIAI_M0089 row: e column: 06
High quality sequence stop:	446.
Location/Qualifiers	
FEATURES	
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/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:439093"	
/clone_lib="NIH_MGC_87"	
/tissue_type="mammary adenocarcinoma, cell line"	
/lab_host="DH10B (phage-resistant)"	
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."	
BASE COUNT	
ORIGIN	163 a . 108 c 132 g 131 t
Query Match	90.3%; Score 482.4; DB 12; Length 534;
Best Local Similarity	98.2%; Pred. No. 2.3e-62;
Matches	499; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
Qy	30 GCGAGAGTAGGGAGGCGGTGCGCCGGCGGGGTGCTATCGCTTCGAGAAC 89
Db	1 GCGAGAGTAGGGAGGCGGTGCGCCGGCGGGGTGCTATCGCTTCGAGAAC 60
Qy	90 CTACTCAGGCCAGCTGAGAAGAGTTAGGGAAAGTGCTGCGCTGGCTCAGACG 149
Db	61 CTACTCAGGCCAGCTGAGAAGAGTTAGGGAAAGTGCTGCGCTGGCTCAGACG 120
Qy	150 CGATGGATAAGCTGAGCCGAATAAACATCGCCCTCTGCTCA3GTGAAAGGCC 209
Db	121 CGATGGATAAGCTGAGCCGAATAAACATCGCCCTCTGCTCA3GTGAAAGGCC 180
Qy	210 ACGTGAGATACTGGCGTGATATATCACTGCTGAAACACAGATTCAGTCGA 269
Db	181 ACGTGAGATACTGGCGTGATTCAGTCGA 240
Qy	270 TCGTACCTGTTGCACTGATACCGAACACACATGACAGTGGGGAGGGT 329
Db	241 TCGTACCTGTTGCACTGATACCGAACACACATGACAGTGGGGAGGGT 300
Qy	330 TTGCACTTGTGACACAGCATGCTGCTGCTGCGACGGGCTTATTACCGGAGCTC 389
Db	301 TTGCACTTGTGACACAGCATGCTGCTGCTGCGACGGGCTTATTACCGGAGCTC 360
Qy	390 TGTCACTCCAGGCTCTTACCGAACAGCTGTGATGAAAGAAGTTG 449
Db	361 TGTTCATCCAGCGCTCTTACCGAACAGCTGTGATGAAAGAAGTTG 420
Qy	450 AATTATATTAATCTTTTGTGATCTAAG -- TATAAACATATTCTGTATCTC 506
Db	421 ATTATATATTAATCTTTTGTGATCTAAG -- TATAAACATATTCTGTATCTC 480
Qy	507 CAAAAA..... 534
Db	481 CCCACAAAAA..... 508
BASE COUNT	139 a 119 c 138 g 133 t
ORIGIN	
Query Match	87.7%; Score 468.2; DB 12; Length 529;
Best Local Similarity	98.2%; Pred. No. 2.9e-60;
Matches	484; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
Qy	23 GAGTTGGAGAGAGTAGGGAGGGGGGGCTCGCGCCCGGGGGGGTGTCTATCGCTTC 82
Db	2 GAGTTGGAGAGAGTAGGGAGGGGGGGCTCGCGCCCGGGGGGGTGTCTATCGCTTC 61
Qy	83 GCAGAACCTACTCAGCACGCCAGCTGAGAAGAGTTAGGGAAAGTGTCTGCTGCTGCTGCT 142
Db	62 GCAGAACCTACTCAGCACGCCAGCTGAGAAGAGTTAGGGAAAGTGTCTGCTGCTGCT 121
Qy	143 GCAGAACCTACTCAGCACGCCAGCTGAGAAGAGTTAGGGAAAGTGTCTGCTGCT 202
Db	122 GCAGAACCTACTCAGCACGCCAGCTGAGAAGAGTTAGGGAAAGTGTCTGCTGCT 181
Qy	203 AAAGGCCACGTGAGATGCTGGCGCTGGATATATCACTACTGTTAACACAGATT 262
Db	182. AAAGGCCACGTGAGATGCTGGCGCTGGATATATCACTACTGTTAACACAGATT 241
Qy	263 ATGGCTATGTTACGTGTTGGACTGTACGAGACACACACATGACAGTGTGTTGA 322
Db	242 ATGGCTATGTTACGTGTTGGACTGTACGAGACACACACATGACAGTGTGTTGA 301
Qy	323 GGGGTGTTGACTGTGAGACAGCAGTAGCTGCTGCTGCTGCGACGGGGCGCCCTTATTACCGG 382
Db	302 GGGGTGTTGACTGTGAGACAGCAGTAGCTGCTGCTGCTGCGACGGGGCGCCCTTATTACCGG 361
Qy	383 AACGTCTGTTCACTCCAGCGCTCTTACCGAACAAAGCCCTGTGATGAAAAAGA - 441
Db	362 AACGTCTGTTCACTCCAGCGCTCTTACCGAACAAAGCCCTGTGATGAAAAAGA - 421
Qy	442 AGTTGTTAATTTACTTTTGTGATCTAGTGTGATTAACATATTCTGT 501
Db	422 AAGTTGTTAATTTACTTTTGTGATCTAGTGTGATTAACATATTCTGT 481
RESULT	7
BF691818	BF691818 529 bp mRNA linear EST 22-Dec-2000
LCUS DEFINITION	60247787F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333244 5'
ACCESSION	mRNA sequence.
VERSION	BF691818.1 GI:11977226
KEYWORDS	human.
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.

Db	61 AGANCTACTCAGGCCAGCCAGTGGAAATAAACATGCCCTTCGCTCGAGCTGAA	204
QY	145
Db	121 AGACCGCATGGATAAAGCTGAGCCGAATAAACATGCCCTTCGCTCGAGCTGAA	204
QY	121
Db	205 AGGCACCTGAAAGTAGTGCTGGGTGGATATTCACTCTCTGTTAACAGTTCA	204
QY	181
Db	181 AGGCACCTGAAAGTAGTGCTGGGTGGATATTCACTCTCTGTTAACAGTTCA	204
QY	205
Db	265 GCTCACGTAATGCTGGTGGACTATACAGAACACACATGGACAGTTGGGAGG	324
QY	265
Db	241 GCTCACGTAATGCTGGTGGACTATACAGAACACACATGGACAGTTGGGAGG	300
QY	241
Db	385 GCTCACGTAATCAGGGTCTTACCGAANAAAGCCTGCTGCAAGAAAAGAAGT	444
QY	385
Db	325 GGTGTTGACTTGAGACAGCTATGCTGCTGCTGGACGGGGCCTTATTACGGAA	384
QY	325
Db	301 GGTG-TTGACTTGAGACAGCTATGCTGCTGCTGGACGGGGCCTTATTACGGAA	359
QY	301
Db	419 TTGTGAATTATATACCTTTAGTTGACTAATGTTAAAGAATTTCTGATTCT	477
QY	419
Db	505 TCCAAAGAAAAAAAGAAAAAAAGAAAAAAAGCTGTCGATGAAAAAAAGAAG-	534
QY	505
Db	478 TCCACAAAGAAAAAAACACAAAAAA 507	534
QY	478
RESULT 10		
LOCUS	A1078580_452 bp mRNA linear EST 10-AUG-1998	
DEFINITION	Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1677561	
ACCESSION		
VERSION	A1078580.1	
KEYWORDS	GI:3412988	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Mammalia; Butheria; Primates; Catarinini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 452) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
JOURNAL	Tumor Gene Index	
COMMENT	Unpublished (1997)	
FEATURES	COMMENT: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 410. Location/Qualifiers	
source	1. .452. /organism="Homo sapiens" /ab_xref="taxon:9606" /clone=IMAGE:1677561" /clone_id="Soares_NHMPU_S1" /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH10B" /note="Organ: Mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of Plasmid DNA from three normalized libraries (melanocyte 2NBH, pregnant uterus NBHU, and fetal heart NBHRGW) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,"	
RESULT 11		
LOCUS	A1743235_453 bp mRNA linear EST 20-DEC-1999	
DEFINITION	wg9a02_xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:272330_3', mRNA sequence.	
ACCESSION	A1743235	
VERSION	A1743235.1	
KEYWORDS	GI:5111523	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarinini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 453) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
JOURNAL	Tumor Gene Index	
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco.	
FEATURES	COMMENT: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov Location/Qualifiers	
source	1. .453. /organism="Homo sapiens" /ab_xref="taxon:9606" /clone=IMAGE:272330" /clone_id="Soares_NSF_F8_9W_OT_PA_P_S1" /lab_host="DH10B" /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;	

Page
8

Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The divisor was

Shanghai Institute of Endocrinology, Rui-Jin Hospital,
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel.: 86-21-64370045 (ex. 6633332)
Fax: 86-21-64712006

PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: The pools consisted of the following libraries and clones: Soares NbHP pool 1: 309394-310915, 322308-325895 Soares NbHP pool 1: -

Fax: 021-54945000
Email: imbhclens.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai, Chinese National Human Genome Center at Shanghai.

Query Match		Best Local Similarity		Score 83.3%; Pred No. 98-9%; Length 453;	
Matches 448; Conservative 0; Mismatches 5; Indels 0; Gaps 0;		Best Local Similarity 98.9%; Pred No. 7-57; Length 453;		/lab_hos="BR25.8"; note="Vector: pntiple2; Site_1: sf1A; Site_2: sf1B"	
QY		61 CGGGGGGGTGCATCGCTTCGAGAACCTACTCAGSCAGCGAGCTGAGAGAGTGAG		120	
Db	453 CGGGGGGGTGCATCGCTTCGAGAACCTACTCAGSCAGCGAGCTGAGAGAGTGAG	394	121 GGAAGTGTGCTGGCTGGCTCGAGACCCGATGAAACGTCAGCCGAAATAAACACA	180	QY
Db	393 GGAAGTGTGCTGGCTGGCTCGAGACCCGATGAAACGTCAGCCGAAATAAACACA	334	181 TCGCCCTCTGCTGCTGAGTGAAAGGCCACGCTGAGAGTGAGCTGCGGTGGATATTACAA	240	QY
Db	333 TCGCCCTCTGCTGCTGAGTGAAAGGCCACGCTGAGAGTGAGCTGCGGTGGATATTACAA	274	301 CACACATGACAGTTGGAGGGGTTGACTGTACGACCAACAAAC	360	QY
Db	241 CTCACTGTTACAAACAGTATTCATGCTCATGCTATGCTGTGTTGACTGTACGACCAACAAAC	300	213 CACACATGACAGTTGGAGGGGTTGACTGTACGACCAACAAAC	154	QY
Db	273 CTCACTGTTACAAACAGTATTCATGCTCATGCTATGCTGTGACTGTACGACCAACAAAC	214	361 CGAGGGGCCCTTAATTACCGAGGCTCTGTCATACTCCACGGGTCTTACAGAAAAAA	420	QY
Db	153 CGAGGGGCCCTTAATTACCGAGGCTCTGTCATACTCCACGGGTCTTACAGAAAAAA	94	421 GCGCTGTCATGAAAAGAGTTTGTAAATTATATACCTTTAGTTGATCTAA	480	QY
Db	93 GCGCTGTCATGAAAAGAGTTTGTAAATTATACCTTTAGTTGATCTAA	34	481 GTATAAACATATTCTGTATTAAAAAA 1	513	QY
Db	33 GTATAAACATATTCTGTATTAAAAAA 1	33	RESULT 12	AV754613	QY
REFERENCE	1 (bases 1 to 533)	533 bp	mRNA	linear EST 19-oct-2000	Db
AUTHORS	Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Ye, M., Zhang, Q., Han, Z., Chen, Z., and Chen, J.	DEFINITION	AV754613 TP Homo sapiens cDNA clone TPAAO11 5', mRNA sequence.	ACCESSION	AV754613
VERSION	AV754613.1	EST.	GI:10912461	KEYWORDS	COMMENT
SOURCE	human.	ORGANISM	Homo sapiens	ORGANISM	Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RESULT 13	AV754613	QY	QY
RESULTS	448 AAAAAGAGAG -- GTAAATTATATACCTTTAGTTGATCTAAGTATAACATA	503	448 AAAAAGAGAG -- GTAAATTATATACCTTTAGTTGATCTAAGTATAACATA	533	Db
DEFINITION	493 TTTCGTATCTTCACAAAAAA 522	Db	493 TTTCGTATCTTCACAAAAAA 522	533	Db
ACCESSION	504 TTTCGTATCTTCACAAAAAA 533	Db	504 TTTCGTATCTTCACAAAAAA 533	533	Db
VERSION	EST.	KEYWORDS	EST.	EST.	ORGANISM
JOURNAL	Unpublished (2000)	TITLE	Homo sapiens TP library cDNA clones	COMMENT	Qinghua Zhang

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 432) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,' Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Scheibenbogen,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.			
TITLE	WasU-Merck EST Project 1997			
JOURNAL	unpublished (1997)			
COMMENT	Contact: Wilson RK			
SOURCE	Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu			
FEATURES	This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq. primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 421. Location/Qualifiers			
	1. 432 '/sex="male" '/lab_host="DH10B" '/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories , Inc., and primed with a Not I - oligo(dT) primer [5', TGTATCACTGAGTGGAGCCGCCCCATTGTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " /db_xref="IMAGE:761291" '/clone_id="Soares_testis_NHT" /organism="Homo sapiens"			
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Query Match	80.6%; Score 430.4; DB 9; Length 432;			
Best Local Similarity	99.8%; Pred. No. 1.3e-54;			
Matches	431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	81 TCGCGAACCTACTCAGGAGCCNGCTGGAAGAGGTGAGGAAGTGTCTGCTGGGT 140			
DB	432 TCGCGAACCTACTCAGGAGCCNGCTGGAAGAGGTGAGGAAGTGTCTGCTGGGT 373			
QY	141 CTGAGACCGATGGATAACGTGGAGCCAAATAAACATCGCCCTTGTCGTCTAGTG 200			
DB	372 CTGCGAACCGATGGATAACGTGGAGCCAAATAAACATCGCCCTTGTCGTCTAGTG 313			
QY	201 TGAAGGCCACGTGAGAAGCTGGCTGATATATCACTCACTGTGACAAAGAT 260			
DB	312 TGAAGGCCACGTGAGAAGCTGGCTGATATATCACTCACTGTGACAAAGAT 253			
QY	261 TCATGCTCATGTTACTGTGTTGCCCCATGACAGTGGTG 320			
DB	252 TCATGCTCATGTTACTGTGTTGCCCCATGACAGTGGTG 193			
QY	321 GAGGGGTGTTGACTGTGACAGCAGTGTGACAGCAAGTGTGCTCTTAC 380			
DB	192 GAGGGGTGTTGACTGTGACAGCAGTGTGACAGCAAGTGTGCTCTTAC 133			
QY	381 GAGGGGTGTTGACTGTGACAGCAGTGTGACAGCAAGTGTGCTCTTAC 440			
DB	132 GGAGCTCTGTGATCCAGCGSGCTCTTACCAAGAAAGCCTGTGCAAGAAAAG 73			
QY	441 AACTTTGTAATTTATTAATCTTTTACTGTACTAAGTATAACATATTCTGT 500			
DB	72 AAGTTTGTAATTTATTAATCTTTTACTGTACTAAGTATAACATATTCTGT 13			
QY	501 TTCTCCAAAAA 512			
BASE COUNT	119 a ORIGIN	119 a 101 c 91 g 116 t		
Query Match	80.0%; Score 427; DB 9; Length 427;			
Best Local Similarity	100.0%; Pred. No. 4.1e-54;			
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DB	427 TCGCGAACCTACTCAGGAGCCAGTGTGAGAAGTGTGAGGAAGTGTCTGCTGGGT 368			
QY	141 CTGAGACGCCATGGATAACGTGGAGCCAAATAAACATCGCCCTTGTCGTCTAGTG 200			
DB	367 CTGAGACGCCATGGATAACGTGGAGCCAAATAAACATCGCCCTTGTCGTCTAGTG 308			
QY	201 TGAAGGCCACGTGAGAAGCTGGCTGCGCTGGTATATCACTCACTGTGACAAAGAT 260			
DB	307 TGAAGGCCACGTGAGAAGCTGGCTGCGCTGGTATATCACTCACTGTGACAAAGAT 248			

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OM protein - nucleic search, using frame_plus_p2n mode

Run on: June 25, 2003, 11:55:49 ; Search time 1313 Seconds
 (without alignments)
 2194.347 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508

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Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

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-DGB=GenEmbl -QFMT=fastaP -MATRIX=blosum62 -TRANS=human40_cdi -LIST=45
-DOCALGN=200 -THR_SCOREP="THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL"
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1	508	100.0	515	6	AF098995 Homo sapi
2	508	100.0	530	9	AF098995 Homo sapi
3	471.5	92.8	655	9	AF057306 Homo sapi
4	471.5	92.8	669	6	AF057306 Homo sapi
5	471.5	92.8	688	9	BC004380 Homo sapi
6	471.5	92.8	689	9	AF135380 Homo sapi
7	366	72.0	485	11	G30204 human STS S
8	339.5	66.8	593	9	AF145216 Homo sapi
9	331	65.2	434	9	AF135381 Homo sapi
10	318.5	62.7	495	6	AX331008 Sequence
11	275	54.1	523	10	AX079335 Sequence
12	245	48.2	207	6	AX330510 Sequence
13	245	48.2	207	6	AX330510 Sequence
14	245	48.2	207	6	AX330510 Sequence
15	245	48.2	207	6	AX408097 Sequence
16	238.5	46.9	682	10	AF253065 Rattus no
17	227.5	44.8	568	10	AY047360 Mus muscu
18	215	42.3	151620	2	AC018589 Homo sapi
19	215	42.3	180702	9	AC018557 Homo sapi
20	215	42.3	188460	9	AC010542 Homo sapi
21	142	28.0	97083	9	AC010589 Homo sapi
22	139.5	27.5	527	10	AY046597 Mus muscu
23	115	22.6	69937	2	AC121275 Mus muscu
24	115	22.6	150552	2	AC121952 Mus muscu
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26	108	21.3	6283	6	AX344330 Sequence
27	108	21.3	6283	6	AX344835 Sequence
28	102	20.1	6283	6	AX252053 Sequence
29	102	20.1	6283	6	AX344331 Sequence
30	102	20.1	6283	6	AX344836 Sequence
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33	86	16.9	159704	2	AC128918 Rattus no
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35	83.5	16.4	792	14	AF105732 HIV-1 iso
36	83.5	16.4	792	14	AF105741 HIV-1 iso
37	83	16.3	37948	6	AR166758 Sequence
38	82.5	16.2	508	10	AF401530 Mus muscu
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ALIGNMENTS

AX061624 AX061624 515 bp DNA linear PAT 24-JAN-2001
LOCUS DEFINITION Sequence 29 from Patent WO0100806.
ACCESSION AX061624
VERSION AX061624.1 GI:12406709
KEYWORDS SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 515)
dumas milne Edwards J.B., Bouqueleret,L. and Jobert,S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 29 04-JAN-2001;
GENSET (FR) location/Organizers
FEATURES source 1..515
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sig_peptide 144..287 /note="Von Heijne matrix score 4.10 seq VFMLIVSVLALLIP/ET"
polya_signal 457..462 /note="Von Heijne matrix score 4.10 seq VFMLIVSVLALLIP/ET"
polyA_site 500..515
BASE COUNT 143 a 106 c 135 g 130 t 1 others
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Alignment scores:
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Score: 500.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 1 METASPASVALGInPROLYSILEYLHSARGPROPHCYSPheservalysGLYHIS 20
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Db 144 ATGGATAACGTGCAAGCCGAATAAACATCGGCCCTTCAGTGTGAAGCCAC 203
QY 21 VALLYSMetLeuAlaLeuAspIleLeasnSerLeuValThrThrValPhenMetLeuIle 40
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Db 204 GTGAGAGAGCTGGCTGCTGATATTACTGACTGTACAGTAATCATGCATC 263
QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuIleValGlyGlyValPhe 60
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db 264 GRATCTGCTGGCACIGTACACAGAACACACATGACGTGGTGGGGGTT 323
BASE COUNT 156 a 108 c 137 g 129 t
ORIGIN
Alignment scores:
Pred. No.: 3.04e-56 Length: 530
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 1 MetAsPAsVALGInPROLYSILEYLHSARGPROPHCYSPheservalysGLYHIS 20
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QY 21 VALLYSMetLeuAlaLeuAspIleLeasnSerLeuValThrThrValPhenMetLeuIle 40
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Db 208 GTGAGAGATGCTGCCGCTGGTAAATTACTGACTGTACAGTGGTGGGGGTT 327
QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuIleValGlyGlyValPhe 60
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Db 268 GRATCTGCTGGCACIGTACACAGAACACATGACGTGGTGGGGGTT 327
QY 61 AlaLeuValThrAlaValCysCysLeuIlaAspGlyAlaLeuIleThrArglyLeuIle 80
324 GCACTTGAGACAGCAGTGTGCTTCGGCAGGGGCCCTTAATTCACGGAACTGTCTG 383
QY 81 PheAsnProSerGlyProTyrglyIlysProvalIhsGluIlysIlysGluValIle 99
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db 384 TCAATCCCAAGCGGTCCTTACCAAGAAAAGCCTGTCATGAAAAAAAGAAGTTG 440
RESULT 2
AF096895 AF096895 530 bp mRNA linear PRI 18-JUL-2001
LOCUS DEFINITION Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.
ACCESSION AF096895
VERSION AF096895.2 GI:9989691
KEYWORDS SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Db	388 TTCAATCCAGGGTCTTACAGAGAAAAACCTGTGATGAAAGAAAGTTTG	444	Db	432 CCAGAACACACATGACAGTGTGAGGGGTTGTGACTTGAGCAGPATGC	491
RESULT	3		QY	68 CysIleuAlaAspIlyAlaLeuIleTyPArglySleuLeuPheAsnProSerGlyProTyR	87
DEFINITION	Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.	655 bp mRNA linear	Db	492 TGCTTGCGACGGGGCCTTAATTACCGGAAGCTCTGTCAATCCAGGGTCCTAC	551
ACCESSION	AF057306	PRI 31-DBC-1999	QY	88 GluLysLysProValHisGluLysLysGluValLeu 99	
VERSION	AF057306.1	GI:6648618	Db		
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ORGANISM	Homo sapiens.				
FEATURES					
source					
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	1 (bases 1 to 655)				
TITLE	Zhang, J.S., Nelson, M., Wang, L. and Smith D.I.				
JOURNAL	Direct Submission				
gene	Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic				
CDS	and Foundation, Rochester, MN 55905, USA				
Location/Qualifiers					
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132 . 590					
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ORIGIN					
Alignment Scores:					
Pred. No.:	1.99e-51				
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Percent Similarity:	65.13%	Matches: 99			
Best local Similarity:	65.13%	Conservative: 0			
Query Match:	92.81%	Mismatches: 0			
DB:	9	Indels: 53			
Gaps:	1				
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OY	21 ValIlysMetLeuArg	25			
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OY	26	-----			
Db	312 CTTTATATGACTCAGCTGATCGATTAATGAACTGTTATTGGCCATTGCTGT	371			
OY	28 IleIleAsnSerIleuValThrThrValPhenLeuIleLeuIleLeuIleLeuIle	47			
Db	372 ATTATCACTCACTGGTACAACAGIATCATCGTACCTGTCAGTGTGCACTGATA	431			
OY	48 ProGluLhrThrIleuThrValGlyGlyGlyIvalPhenLeuLeuValThrAlaValCys	67			
Db					
OY	26 -----				
Db	320 CTTTATAATGACTCAGACTGTGATCGATTAATGAGTGTGTTATTGGCCATTGCTGT	379			
OY	28 IleIleAsnSerIleuValThrThrValPhenLeuIleLeuIleLeuIleLeuIle	47			

Db	380 ATTCACACTCACTGGTAAACAACAGATTCATGCTCATCGTACATCGTTGCCACTGATA	439	ORIGIN
Qy	48 ProglutathrthrLeuthrvalgylglylvalpheAaleuvalthAlaValCys	67	Alignment Scores:
Db	440 CCAGAACACACACATGACAGTGAGGGGGTTGCACATGAGCACAGATGC	499	Pred. No.: 2.11e-51
Qy	68 CysLeuAlaAspGlyAlaLeuLeuLtyArglyLeuLeuPheAsnProSerGlyProY	87	Length: 688
Db	500 TGCTTGCGACGGGCCCTTAATACCGGAAGCTGTCAATCCACGGTCCTTAC	559	Matches: 99
Qy	88 GlnLySlysProValHisGluLySlysGluValLeu	99	Percent Similarity: 65.13%
Db	560 CAGAAAAGCCCTGCGATGAAAAAAAGAAGTTTG	595	Best Local Similarity: 65.13%
RESULT 5	BC004380	688 bp mRNA linear	PRI 12-JUL-2001
REFERENCE	BC004380	mRNA, complete cds.	
AUTHORS	Homo sapiens, clone MGC:10658		
LOCUS	BC004380		
DEFINITION	Homo sapiens, clone MGC:10658		
ACCESSION	BC004380		
VIRSION	BC004380.1		
KEYWORDS	Glucosidase		
SOURCE	MGC.		
ORGANISM	Homo sapiens.		
Bukay-Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REMARK	1 (bases 1 to 688)		
1. Strausberg, R.			
TITLE	Direct Submission		
JOURNAL			
COMMENT	Submitted (12-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
NTH-MGC Project URL:	http://mgc.nci.nih.gov		
Contact:	MGC help desk		
Email:	cgbps-r@mail.nih.gov		
Tissue Procurement:	ATCC		
DNA Library Preparation:	Robin Laboratory		
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)		
DNA Sequencing by:	Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada		
Info@bcsc.bc.ca			
Steven Jones, Jennifer Asano, Ian Boshet, Yaron Butterfield, Susanna Chan, Reuben Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzivinski, Neta Kutsche, Oliver Lee, Soo Ness, Pawan Pandoh, Carrie Mathewson, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsui, Natasha van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.			
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
Series:	IRL Plate: I3 Row: F Column: 14		
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9989692.			
Location/Qualifiers			
FEATURES			
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Qy	21 ValysMetLeuArg-----	25	
Db	197 GTGAGAGATGCTGCGCCGCTGCACTACTGTGACATCTATGACCTTTTATCATCGCACAA	256	
Qy	25 -----	25	
Db	257 GCCCTGAACCATAATATGTTATCATGATGGATTGAGTCACCGTTACTTATTTCATCA	316	
Qy	26 -----	LeuASP 27	
Db	317 CTTTATATGACTGAGCTGATGATGAAATGAGTGTTGCCTTGCTGTGAT	376	
Qy	28 IleLeuAsnSerLeuValThrThrValhemeMetLeuLeuValSerValLeuAlaLeuLe	47	
Db	377 ATTACACTCACGGTAAACACAGATTCATGCTCATCGTACATCGTCTGTTGCGACAGATA	439	
Qy	48 ProglutathrthrLeuLeuLtyArglyLglylvalpheAaleuvalthAlaValCys 67		
Db	497 TGCTTGCGACGGGCCCTTAATACCGGAAGCTGTCAATCCACGGTCCTTAC	559	
Qy	437 CCAGAACACACATGACAGTGAGGAGGGGTTGACTGTGACAGCAGATGC 496		
Db	557 CAGAAAAGCCCTGCGATGAAAAAAAGAAGTTTG	592	
RESULT 6	AF135380	689 bp mRNA linear	PRI 07-SEP-2000
REFERENCE	AF135380	Homo sapiens chemokine-like factor 2 (CKLF2) mRNA, complete cds,	
ACCESSION	AF135380	alternatively spliced.	
VERSION	AF135380.2		
KEYWORDS	GI:9989692		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
Bukay-Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REMARK	1 (bases 1 to 689)		
REFERENCE	Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D.		
AUTHORS	Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China		
TITLE	Sequence update by submitter		
JOURNAL	On Sep 7, 2000 this sequence version replaced gi:6630853.		
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148 . 606
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BASE COUNT 195 a 140 c 161 g 193 t
ORIGIN

Alignment Scores:
Pred. No.: 2.11e-51 Length: 689
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF135380 (1-689)

Qy 1 MetAspAsnValGlnInProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 148 ATGGATAAGCTGGAGCCGAATAACATCGCCCTTCCTGCAGTGAAAGGCCAC 207

Qy 21 ValIysMetLeuArg----- 25
Db 203 GTGAGAGATCCTGGGGCTGCACTACTGTGACATCTATGACCTTTTATCATCGCACAA 267

Qy 25 ----- 25
Db 268 GCCCTGAAACCATATATTGTTACACTGAGTTGAAGTGTCAACCGTATCTTATTCATA 327

Qy 26 -----LeAsp 27
Db 328 CTTTATATGTACTCAGACTTGATCGATTATGAAAGTGTGTTATTGCTCTTGCTGAT 387

Qy 28 IleLeAsnSerLeuValThrValPheMetIleIleValSerValLeuAlaLeuIle 47
Db 388 ATTATCACTCAGCTAACACAGTATCTCATGTAATCTGTGTTGGCACTGATA 447

Qy 48 ProGluThrThrLeuThrValIgLyIgLyIgLyValPheAlaLeuValThrAlaValCys 67.

Db 448 CCAGAAACCCACATGACAGTGGGGGTGTTGACTGTCAACAGCATGTC 507

Qy 68 CysteuaIaAspGlyIaIaLeuIleTyraRgLySleuLeuPheasnProSerGlyProTy 87
Db 503 TGTCTGCGACGGGGCTTATTACGGAACTCTCTGTCATCCAGGGCTTAC 567

Qy 88 GlnIysLysProValHisGluLysGluValLeu 99
Db 568 CAGAAAAGCTGCGAAGAAAAAGAGTTTG 603

RESULT 7
G30204/c LOCUS G30204 485 bp DNA linear STS 05-OCT-1996
DEFINITION human STS SHGC-36487, sequence tagged site.
ACCESSION G30204
VERSION 1 GI:1593755
KEYWORDS SITS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 485)
AUTHORS Myers, R.M.
JOURNAL Unpublished (1996)

COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 415/7259687
Fax: 415/7259689
Email: myers@shgc.stanford.edu

Primer A: ACTCTTCTTTTCATGACAGG
Primer B: GCCCTTATTACGGGAACT
STS size: 77

PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng each 1 uM
Primer: DNTPS: 0.05 units/uL
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL

FEATURES
source
BASE COUNT 146 a 99 c 99 g 131 t 10 others
ORIGIN
Alignment Scores:
Pred. No.: 5.4e-38 Length: 485
Score: 366.00 Matches: 73
Percent Similarity: 98.658 Conservative: 0
Best Local Similarity: 98.658 Mismatches: 1
Query Match: 72.058 Indels: 0
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x G30204 (1-485)

Qy 26 LeuAspIleAsnSerLeuValThrValPheMetIleIleValSerValLeuAla 45
Db 286 CTGAAATTATCACTCACTGTAACAACTGATGCACTGTCATGTGTAACAGTGTGTTGGCA 227

Qy 46 IleLeProGluThrThrLeuLeuIleIleValPheAlaLeuValThrAla 65
Db 226 CTGATACAGAAACCCACACATGACAGTGGTGGGGGTTGACAGTGTGACGACA 167

Qy 66 ValCysCysLeuIaAspGlyIaIaLeuIleTyraRgLySleuLeuPheasnProSerGly 85
Db 166 GTATGGTGTCTGCGACGGGGCTTATTACGGAACTCTCTGTCATCCAGGGT 107

Qy 86 ProTyGlnIysLysProValHisGluLysGluValLeu 99
Db 106 CCTTACAGAAAAGCTGTCATGAAAGAGTTTG 65

RESULT 8

AFL45216 AFL45216 593 bp mRNA linear PRI 07-SEP-2000
LOCUS DEFINITION Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,
alternatively spliced.

ACCESSION AFL45216
VERSION AFL45216_2 GI:9989694
KEYWORDS SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS Han,W.L., Gu,W.F., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L.
TITLE JOURNAL Direct Submission
Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China
REFERENCE AUTHORS Han,W.L.
TITLE JOURNAL Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK On SEP 7, 2000 this sequence version replaced gi:6625671.
FEATURES source
1. . 593
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
gene
1. . 593
/gene="CKLF4"
/note="UCK"
148. . 510
/gene="CKLF4"
/note="UCK-4; alternatively spliced"
/codon_start=1
/product="chemokine-like factor 4"
/protein_id="AAFI9350_1"
/db_xref="GI:6625672"
/translation="MDNQPKIHRPRCFSVKGHVKMLRLALTVTSMTFRIQAPEP YLVTSEPVTLIFLFLYVRLDRMKWLWPLNFALVTFAVCLADGALIYRLLF NPSGPYQKPKVHEKKEVL"

BASE COUNT ORIGIN 166 a 120 C 140 G 167 t

Alignment Scores:
Pred. No.: 1.79e-34 Length: 593
Score: 339.50 Matches: 73
Percent Similarity: 61.90% Conservative: 5
Best Local Similarity: 57.94% Mismatches: 15
Query Match: 66.83% Indels: 33
DB: 9 Gaps: 2

US-09-801-115B-2 (1-99) x AFL45216 (1-593)

QY 1 MetaspasValGlnProLysIleLysIleArgProPhiCysPhiSerValLysGlyHis 20
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 148 ATGGATAACGTGCAGCCGAATTAACATGCCCTCTGCTCACTGAAAGCCAC 207
QY 21 ValLysMetLeuArgLeuAspIleAspLeuSerLeuValThrThrValPhemLeuLe 40
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 208 GTGAAGATGCTGCGCTGGCACTA 249
QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyGly---- 58
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 TTTTGTATCATGGCACACAAGCCCCGGAACATATATTGTATCATCTGGATTGAGTCACC 309
QY 58 ----- 58
Db 310 GTTATCTTATTTCTATCTTATCTCTACTGAGCTGTGATGTATPATGAAGTGGTA 369
QY 59 ----- ValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAla 73

REFERENCE AUTHORS Han,W.L., Gu,W.F., Li,Y., Zhang,Y.M., Song,Q.S. and Ma,D.L.
TITLE JOURNAL Direct Submission
Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China
REFERENCE AUTHORS Han,W.L.
TITLE JOURNAL Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK On Sep 7, 2000 this sequence version replaced gi:6630855.
FEATURES source
1. . 434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
1. . 434
/gene="CKLF3"
/note="UCK"
148. . 351
/gene="CKLF3"
/note="UCK-3; alternatively spliced"
/codon_start=1
/product="chemokine-like factor 3"
/protein_id="AAFI9600_1"
/db_xref="GI:6630856"
/translation="MDNQPKIHRPRCFSVKGHVKMLRLALTVTSMTFRIQAPEP RKLUENPSGPYQKPKVHEKKEVL"

BASE COUNT ORIGIN 127 a 88 c 116 g 103 t

Alignment Scores:
Pred. No.: 1.52e-33 Length: 434
Score: 331.00 Matches: 67
Percent Similarity: 67.68% Conservative: 0
Best Local Similarity: 67.68% Mismatches: 0
Query Match: 65.16% Indels: 32
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF135381 (1-434)

QY 1 MetaspasValGlnProLysIleLysIleArgProPhiCysPhiSerValLysGlyHis 20
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 148 ATGGATAACGTGCAGCCGAATTAACATGCCCTCTGCTCACTGAAAGCCAC 207
QY 21 ValLysMetLeuArgLeuAspIleAspLeuSerLeuValThrThrValPhemLeuLe 40
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 208 GTGAAGATGCTGCGCTGGCACTA 249
QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyGly---- 58
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 TTTTGTATCATGGCACACAAGCCCCGGAACATATATTGTATCATCTGGATTGAGTCACC 309
QY 58 ----- 58
Db 310 GTTATCTTATTTCTATCTTATCTCTACTGAGCTGTGATGTATPATGAAGTGGTA 369
QY 59 ----- ValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAla 73

REFERENCE AUTHORS Han,W.L., Gu,W.F., Li,Y., Zhang,Y.M., Song,Q.S. and Ma,D.L.
TITLE JOURNAL Direct Submission
Submitted (07-SEP-2000) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China
REFERENCE AUTHORS Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D.
TITLE JOURNAL Direct Submission
Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China
REFERENCE AUTHORS Han,W.L.
TITLE JOURNAL Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK On Sep 7, 2000 this sequence version replaced gi:6630855.
FEATURES source
1. . 434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
1. . 434
/gene="CKLF3"
/note="UCK"
148. . 351
/gene="CKLF3"
/note="UCK-3; alternatively spliced"
/codon_start=1
/product="chemokine-like factor 3"
/protein_id="AAFI9600_1"
/db_xref="GI:6630856"
/translation="MDNQPKIHRPRCFSVKGHVKMLRLALTVTSMTFRIQAPEP RKLUENPSGPYQKPKVHEKKEVL"

BASE COUNT ORIGIN 127 a 88 c 116 g 103 t

Alignment Scores:
Pred. No.: 1.52e-33 Length: 434
Score: 331.00 Matches: 67
Percent Similarity: 67.68% Conservative: 0
Best Local Similarity: 67.68% Mismatches: 0
Query Match: 65.16% Indels: 32
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF135381 (1-434)

QY 1 MetaspasValGlnProLysIleLysIleArgProPhiCysPhiSerValLysGlyHis 20
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 148 ATGGATAACGTGCAGCCGAATTAACATGCCCTCTGCTCACTGAAAGCCAC 207
QY 21 ValLysMetLeuArgLeuAspIleAspLeuSerLeuValThrThrValPhemLeuLe 40
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 208 GTGAAGATGCTGCGCTGGCACTA 249
QY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyGly---- 58
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 TTTTGTATCATGGCACACAAGCCCCGGAACATATATTGTATCATCTGGATTGAGTCACC 309
QY 58 ----- 58
Db 310 GTTATCTTATTTCTATCTTATCTCTACTGAGCTGTGATGTATPATGAAGTGGTA 369
QY 59 ----- ValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAla 73

QY	41	ValSerValLeuAlaLeuIleProGluthrThrThrLeuThrValGlyGlyGlyValPhe 60		AF253064	AF253064	523 bp mRNA	linear	ROD 27-Nov-2001
Db	226	-----	-----	LOCUS	Rattus norvegicus	chemokine-like factor 1 (CKLF1) mRNA, complete cds		
QY	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyValAlaLeuIleTyrArgLysLeu 80		DEFINITION	AF253064			
Db	232	GCACITGGCACAGCAGTCATGCTCTGCCGAGGGCCCTATTACCGAAGCTCTG 291		ACCESSION	AF253064.2	GI:17105378		
QY	81	PheAsnProSerglyProTyroGlnLysLysProValHisGluLysLysGluValLeu 99		VERSION				
Db	292	TCATACCCAGCGTCTTACCGAAGAAAGCCGCTGTGATGAAAGAAAAGAAGTTG 348		KEYWORDS				
RESULT	10	-----	-----	SOURCE	Rattus norvegicus			
Ax079435				ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
LOCUS	AX079435	495 bp DNA	linear	REFERENCE	1 (bases 1 to 533)			
DEFINITION	Sequence 179 from Patent WO0107611.			AUTHORS	Lou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.			
ACCESSION	AX079435			TITLE	Direct Submission			
VERSION				JOURNAL	Submitted (08-APR-2000) Immunology, Beijing Medical University, Xueyuan Road, Beijing 100083, China			
KEYWORDS					2 (bases 1 to 533)			
SOURCE								
ORGANISM								
REFERENCE								
1	(bases 1 to 495)							
AUTHORS	Baker, K.P., Goddard, A. and Wood, W.I.							
TITLE	Human polypeptides and methods for the use thereof							
JOURNAL	Patent: WO 0107611-A 179 01-FEB-2001; Genentech, Inc. (US);							
FEATURES	Location/Qualifiers							
source	1..495							
/organism="Homo sapiens"								
/db_xref="Taxon:9606"								
BASE COUNT	119 a 103 c 127 g 142 t 4 others							
ORIGIN								
Alignment Scores:								
Pred. No.:	7..3e-32	Length:	495					
Score:	3.0e-50	Matches:	70					
Percent Similarity:	56.45%	Conservative:	0					
Best Local Similarity:	56.45%	Mismatches:	1					
Query Match:	62.70%	Indels:	53					
DB:		Gaps:	1					
US-09-801-115B-2 (1-99) x AX079435 (1-495)								
QY	1	METASPASnValGlnProLySleIleLysHisArgProHeCysPheSerValLysGlyHis 20		BASE COUNT	134 a 107 c 133 g 149 t			
Db	124	ATGGATAAACGTGCAAGCCAAATAAACATCGCCCCCTCTGCTCAGTGAAAGCCAC 183		ORIGIN				
QY	21	ValIlysMetLeuArg----- 25		Alignment Scores:				
Db	184	GTGAGAGCTGGCGCAGCACTAACCTGNGACATCTATGACCTTTATNATGCCACAA 243		Pred. No.:	3.14e-26	Length:	523	
QY	25	----- 25		Score:	275.00	Matches:	53	
Db	244	GCCCCTGACCATATAATGTTACTGAGTTGAAGTCACCGTTATCTTTCATA 303		Percent Similarity:	76.67%	Conservative:	16	
QY	26	-----LeuAsp 27		Best Local Similarity:	58.89%	Mismatches:	21	
Db	304	CTTGTATGATGTCAGCTGATGCTTAATGAAAGTGTTAATGCTGCTGAT 363		Query Match:	54.13%	Indels:	0	
QY	28	IleLeuAsnSerLeuValThrIleValPhenMetLeuIleValSerValLeuAlaLeuIle 47		DB:	10	Gaps:	0	
Db	364	ATTCATCACTCAGCTGTAACAGTATCAGTCATGCTGATCTGCTGACTGATA 423		US-09-801-115B-2 (1-99) x AF253064 (1-523)				
QY	48	ProGluIleThrIleIleLeuAlaLeuValThrAlaValCysCys 67		QY	1	MetaspasnValGlnProLySleIleLysHisArgProHeCysPheSerValLysGlyHis 20		
Db	424	CCAGAACACCAACATGAGCTGAGCTGGGAGGGGTITGACTIGACAGCAGTAGTC 483		Db	167	ATGGACCTCTCCACAGAGGCTGACCCATCAGGCCCTCGCCAGCTGCTGAT 226		
QY	68	CysteauAlaAsp 71		QY	21	ValIlysMetLeuArgLeuAspIleLeuAsnSerLeuValThrIleValPhenMetLeuIle 40		
Db	484	TGTNTTGCGAC 495		Db	227	GGAGAGCGCTGGTGGGTTACACTCGGGTGTACACTATCATGCTT 286		
QY	81	PhesAsnProSerglyProTyroGlnLysLys 90		QY	41	ValSerValLeuAlaLeuIleProGluthrThrThrLeuThrValGlyGlyGlyValPhe 60		
Db				Db	287	GGTCTGCTGCGCTTAATACCAAAACCCACAAATGATAATGCTGAGGGTGTG 346		
QY				Db	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyValAlaLeuIleTyrArgLysLeu 80		
Db				Db	347	GCTTCCTGAGTAATGACTGATGCTGATGCTGATGCTGAGAAACTCCG 406		
QY				QY				

||||||| ||||| ||||| ||||| |||||
Db 407 TTTGGTCCACATGGACCTTATCAGAACAGG 436

RESULT 12
AX330610/c

LOCUS AX330610 207 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 1119 from Patent WO0194629.

ACCESSION AX330610

VERSION AX330610.1 GI:1810588

KEYWORDS

SOURCE

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.

TITLE Cancer gene determination and therapeutic screening using signature gene sets

JOURNAL Patent: WO 0194629-A 1119 13-DEC-2001;

FEATURES

source

1. .207
/organism="Homo sapiens"
/ab_xref="taxon:9606"
BASE COUNT 70 a 43 c 39 g 54 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 7.42e-23 **Length:** 207

Score: 245.00 **Matches:** 47
Percent Similarity: 97.92% **Conservative:** 0
Best Local Similarity: 97.92% **Mismatches:** 1
Query Match: 68.23% **Indels:** 0
DB: 6 Gaps: 0

US-09-801-115B-2 (1-99) x AX330610 (1-207)

RESULT 14
AX331008/c

LOCUS AX331008 207 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 1517 from Patent WO0194629.

ACCESSION AX331008

VERSION AX331008.1 GI:18121642

KEYWORDS

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.

TITLE Cancer gene determination and therapeutic screening using signature gene sets

JOURNAL Patent: WO 0194629-A 1517 13-DEC-2001;

FEATURES

source

1. .207
/organism="Homo sapiens"
/ab_xref="taxon:9606"
BASE COUNT 70 a 43 c 39 g 54 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 7.42e-23 **Length:** 207

Score: 245.00 **Matches:** 47
Percent Similarity: 97.92% **Conservative:** 0
Best Local Similarity: 97.92% **Mismatches:** 1
Query Match: 68.23% **Indels:** 0
DB: 6 Gaps: 0

US-09-801-115B-2 (1-99) x AX331008 (1-207)

RESULT 15
AX408097/c

LOCUS AX330787 207 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 1296 from Patent WO0194629.

ACCESSION AX330787

VERSION AX330787.1 GI:18103765

KEYWORDS

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.

TITLE Cancer gene determination and therapeutic screening using signature gene sets

JOURNAL Patent: WO 0194629-A 1296 13-DEC-2001;

FEATURES

source

1. .207
/organism="Homo sapiens"
/ab_xref="taxon:9606"
BASE COUNT 70 a 43 c 39 g 54 t 1 others
ORIGIN

LOCUS AX408097
DEFINITION Sequence 744 from Patent WO229103.
ACCESSION AX408097
VERSION AX408097.1 GI:21440802
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Alvares,C., Horne,D., Peres da-Silva,S. and Vockley,J.G.
JOURNAL Gene expression profiles in liver cancer
PATENT WO 0229103-A 744 11-APR-2002;
GENE LOGIC INC (US)
FEATURES source
location/qualifiers
 1..207
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. AA338760"

BASE COUNT 70 a 43 c 39 g 54 t
ORIGIN 1 others

Alignment Scores:

Ped. No.: 7.42e-23 **Length:** 207
Score: 245.00 **Matches:** 47
Percent Similarity: 97.92% **Conservative:** 0
Best Local Similarity: 97.92% **Mismatches:** 1
Query Match: 48.23% **Indels:** 0
DB: 6 **Gaps:** 0

US-09-801-115B-2 (1-99) x AX408097 (1-207)

QY	52	ThrIlethrValGlyGlyGlyValPheAlaLeuValThrAlaValCysCysLeuAlaAsp	71
DB	205	ACATTGGAGCTTGTTGCGAGGTGTTGCACTTGTCACAGTATGCCCTGCCTGCCAC	146
QY	72	GlyAlaLeuIleValGlyLysLeuLeuPheAsnProSerGlyProTyroGlyLysLeuAsp	91
DB	145	GGGCCTTATTTACCGAAGCTCTGTCATCCAGCGGCCCTACAGNAAGCT	86
QY	92	ValHisGluLysGluValLeu	99
DB	85	GTCATGAAATAAAGAGTGTG	62

Search completed: June 25, 2003, 13:13:15
 Job time : 1316 secs

